



## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: FENG, YIQING  
BAUM, CHARLES M  
CAPARON, MAIRE H  
ZURFLUH, LINDA L  
KLEIN, BARBARA K  
MCWHERTER, CHARLES A  
STATEN, NICHOLAS R  
SUMMERS, NEENA L  
BAUER, S C  
LEE, STEPHEN C
- (ii) TITLE OF INVENTION: MULTI-FUNCTIONAL HEMATOPOIETIC  
FUSION PROTEINS BETWEEN SEQUENCE REARRANGED  
G-CSF RECEPTOR AGONISTS AND OTHER  
HEMATOPOIETIC FACTORS
- (iii) NUMBER OF SEQUENCES: 313
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: CAROL M. NIELSEN, GARDERE WYNNE SEWELL, LLP
  - (B) STREET: 1000 LOUISIANA, SUITE 3400
  - (C) CITY: HOUSTON
  - (D) STATE: TEXAS
  - (E) COUNTRY: USA
  - (F) ZIP: 77002-5007
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US/10/695,584
  - (B) FILING DATE: 27-Oct-2003
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/510,238
  - (B) FILING DATE: 22-FEB-2002
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/835,162
  - (B) FILING DATE: 04-APR-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO PCT/US 96/15774
  - (B) FILING DATE: 06-OCT-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/004,834
  - (B) FILING DATE: 05-OCT-1995

(viii) ATTORNEY/AGENT INFORMATION:  
    (A) NAME: NIELSEN, CAROL M  
    (B) REGISTRATION NUMBER: 37,676  
    (C) REFERENCE/DOCKET NUMBER: 2910/3

(ix) TELECOMMUNICATION INFORMATION:  
    (A) TELEPHONE: 713-276-5383  
    (B) TELEFAX: 713-276-5383

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 174 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 1  
    (D) OTHER INFORMATION: /note= "Xaa at position 1 is Thr,  
Ser, Arg, Tyr or Gly;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 2  
    (D) OTHER INFORMATION: /note= "Xaa at position 2 is Pro or  
Leu;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 3  
    (D) OTHER INFORMATION: /note= "Xaa at position 3 is Leu,  
Arg, Tyr or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 13  
    (D) OTHER INFORMATION: /note= "Xaa at position 13 is Phe,  
Ser, His, Thr or Pro;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 16  
    (D) OTHER INFORMATION: /note= "Xaa at position 16 is Lys,  
Pro, Ser, thr or His;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 17  
    (D) OTHER INFORMATION: /note= "Xaa at position 17 is Cys,  
Ser, Gly, Ala, Ile, Tyr or Arg;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 18  
    (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,  
Thr, Pro, His, Ile or Cys;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 22  
    (D) OTHER INFORMATION: /note= "Xaa at position 22 is Arg,  
Tyr, Ser, Thr or Ala;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 24  
    (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,  
Pro, Tyr or Leu;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 27  
    (D) OTHER INFORMATION: /note= "Xaa at position 27 is Asp,  
or Gly;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 30  
    (D) OTHER INFORMATION: /note= "Xaa at position 30 is Ala,  
Ile, Leu or Gly;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 34  
    (D) OTHER INFORMATION: /note= "Xaa at position 34 is Lys  
or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 36  
    (D) OTHER INFORMATION: /note= "Xaa at position 36 is Cys  
or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 42  
    (D) OTHER INFORMATION: /note= "Xaa at position 42 is Cys  
or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 43  
    (D) OTHER INFORMATION: /note= "Xaa at position 43 is His,  
Thr, Gly, Val, Lys, Trp, Ala, Arg, Cys, or Leu;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site

(B) LOCATION: 44  
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Pro,  
Gly, Arg, Asp, Val, Ala, His, Trp, Gln, or Thr;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 46  
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Glu,  
Arg, Phe, Arg, Ile or Ala;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 47  
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Leu  
or Thr;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 49  
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Leu,  
Phe, Arg or Ser;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 50  
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Leu,  
Ile, His, Pro or Tyr;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 54  
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu  
or His;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 64  
(D) OTHER INFORMATION: /note= "Xaa at position 64 is Cys  
or Ser;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 67  
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Gln,  
Lys, Leu or Cys;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 70  
(D) OTHER INFORMATION: /note= "Xaa at position 70 is Gln,  
Pro, Leu, Arg or Ser;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 74  
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Cys  
or Ser;"



(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 104  
    (D) OTHER INFORMATION: /note= "Xaa at position 104 is Asp,  
Gly or Val;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 108  
    (D) OTHER INFORMATION: /note= "Xaa at position 108 is Leu,  
Ala, Val, Arg, Trp, Gln or Gly;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 115  
    (D) OTHER INFORMATION: /note= "Xaa at position 115 is Thr,  
His, Leu or Ala;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 123  
    (D) OTHER INFORMATION: /note= "Xaa at position 123 is Glu,  
Arg, Phe or Thr"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 144  
    (D) OTHER INFORMATION: /note= "Xaa at position 144 is Phe,  
His, Arg, Pro, Leu, Gln or Glu;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 146  
    (D) OTHER INFORMATION: /note= "Xaa at position 146 is Arg  
or Gln;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 147  
    (D) OTHER INFORMATION: /note= "Xaa at position 147 is Arg  
or Gln;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 156  
    (D) OTHER INFORMATION: /note= "Xaa at position 156 is His,  
Gly or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 159  
    (D) OTHER INFORMATION: /note= "Xaa at position 159 is Ser,  
Arg, Thr, Tyr, Val or Gly;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site

(B) LOCATION: 162  
(D) OTHER INFORMATION: /note= "Xaa at position 162 is Glu,  
Leu, Gly or Trp;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 163  
(D) OTHER INFORMATION: /note= "Xaa at position 163 is Val,  
Gly, Arg or Ala;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 169  
(D) OTHER INFORMATION: /note= "Xaa at position 169 is Arg,  
Ser, Leu, Arg or Cys;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 170  
(D) OTHER INFORMATION: /note= "Xaa at position 170 is His,  
Arg or Ser;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa	Xaa	Xaa	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Xaa	Leu	Leu	Xaa
1				5					10					15	
Xaa	Xaa	Glu	Gln	Val	Xaa	Lys	Xaa	Gln	Gly	Xaa	Gly	Ala	Xaa	Leu	Gln
		20						25					30		
Glu	Xaa	Leu	Xaa	Ala	Thr	Tyr	Lys	Leu	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Val
		35					40					45			
Xaa	Xaa	Gly	His	Ser	Xaa	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Xaa
		50				55				60					
Pro	Ser	Xaa	Ala	Leu	Xaa	Leu	Ala	Gly	Xaa	Leu	Ser	Gln	Leu	His	Ser
65				70					75					80	
Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser
			85					90						95	
Pro	Glu	Leu	Gly	Pro	Thr	Leu	Xaa	Thr	Leu	Gln	Xaa	Asp	Val	Ala	Asp
		100						105					110		
Phe	Ala	Xaa	Thr	Ile	Trp	Gln	Gln	Met	Glu	Xaa	Leu	Gly	Met	Ala	Pro
		115				120						125			
Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Xaa
		130				135					140				
Gln	Xaa	Xaa	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	Xaa	Leu	Gln	Xaa	Phe
145				150					155					160	
Leu	Xaa	Xaa	Ser	Tyr	Arg	Val	Leu	Xaa	Xaa	Leu	Ala	Gln	Pro		
				165					170						

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 17
  - (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 18
  - (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 19
  - (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 20
  - (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 21
  - (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 22
  - (D) OTHER INFORMATION: /note= "Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 23
  - (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 24

(D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, Leu;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 25

(D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 26

(D) OTHER INFORMATION: /note= "Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, Trp;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 27

(D) OTHER INFORMATION: /note= "Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 28

(D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 29

(D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 30

(D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or L..."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 31

(D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 32

(D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 33

(D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 34  
 (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,  
Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 35  
 (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,  
Ala, Gly, Asn, Pro, Gln, or Val;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 36  
 (D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp,  
Leu, or Val;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 37  
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,  
Ser, Pro, Trp, or Ile;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 38  
 (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,  
or Ala;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 40  
 (D) OTHER INFORMATION: /note= "Xaa at position 40 is Leu,  
Trp, or Arg;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 41  
 (D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn,  
Cys, Arg, Leu, His, Met, or pro;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 42  
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,  
Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met  
or Ala;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 43  
 (D) OTHER INFORMATION: /note= "Xaa at position 43 is Glu,  
Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly, or Ser;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site

(B) LOCATION: 44  
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp,  
Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 45  
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,  
Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala,  
Ile, Glu or His;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 46  
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,  
Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val  
or Gly;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 47  
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile,  
Gly, Val, Ser, Arg, Pro, or His;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 48  
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Leu,  
Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or  
Asn;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 49  
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,  
Arg, Ala, Gly, Pro, Asn, His, or Asp;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 50  
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,  
Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met  
or Gln;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 51  
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,  
Arg, Met, Pro, Ser, Thr, or his;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 52  
(D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn,  
His, Arg, Leu, Gly, Ser, or Thr;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 53  
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Leu,  
Thr, Ala, Gly, Glu, Pro, Lys, Ser, or M..."

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 54  
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg,  
Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 55  
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,  
Thr, Val, Ser, Leu, or Gly;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 56  
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,  
Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val  
or Lys;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 57  
 (D) OTHER INFORMATION: /note= "Xaa at position 57 is Asn  
or Gly;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 58  
 (D) OTHER INFORMATION: /note= "Xaa at position 58 is Leu,  
Ser, Asp, Arg, Gln, Val, or Cys;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 59  
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu,  
Tyr, His, Leu, Pro, or Arg;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 60  
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala,  
Ser, Pro, Tyr, Asn, or Thr;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 61  
 (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe,  
Asn, Glu, Pro, Lys, Arg, or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 62  
    (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,  
His, Val, Arg, Pro, Thr, Asp, or Ile;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 63  
    (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg,  
Tyr, Trp, Lys, Ser, His, Pro, or Val;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 64  
    (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala,  
Asn, Pro, Ser, or Lys;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 65  
    (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val,  
Thr, Pro, His, Leu, Phe, or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 66  
    (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys,  
Ile, Arg, Val, Asn, Glu, or Ser;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 67  
    (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser,  
Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 68  
    (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
Val, Trp, Ser, Ile, Phe, Thr, or His;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 69  
    (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,  
Ala, Pro, Thr, Glu, Arg, Trp, Gly, or L..."

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 70  
    (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn,  
Leu, Val, Trp, pro, or Ala;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 71



(D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 72

(D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 74

(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 75

(D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 76

(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or A..."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 77

(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 78

(D) OTHER INFORMATION: /note= "Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 79

(D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 80

(D) OTHER INFORMATION: /note= "Xaa position at 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 81  
    (D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu,  
Gln, Gly, Ala, Trp, Arg, Val, or Lys;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 82  
    (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,  
Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe,  
Ile, Met or Val;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 83  
    (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro,  
Ala, Thr, Trp, Arg, or Met;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 84  
    (D) OTHER INFORMATION: /note= "Xaa at position 84 is Cys,  
Glu, Gly, Arg, Met, or Val;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 85  
    (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu,  
Asn, Val, or Gln;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 86  
    (D) OTHER INFORMATION: /note= "Xaa at position 86 is Pro,  
Cys, Arg, Ala, or Lys;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 87  
    (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu,  
Ser, Trp, or Gly;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 88  
    (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala,  
Lys, Arg, Val, or Trp;"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 89  
    (D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr,  
Asp, Cys, Leu, Val, Glu, His, Asn, or S..."

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 90  
(D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala,  
Pro, Ser, Thr, Gly, Asp, Ile, or ,Met;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 91  
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala,  
Pro, Ser, Thr, Phe, Leu, Asp, or His;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 92  
(D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro,  
Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 93  
(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,  
Asp, Ser, Asn, Pro, Ala, Leu, or Arg;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 94  
(D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,  
Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 95  
(D) OTHER INFORMATION: /note= "Xaa at position 95 is His,  
Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe,  
Ile, or Tyr;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 96  
(D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro,  
Lys, Tyr, Gly, Ile, or Thr;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 97  
(D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile,  
Val, Lys, Ala, or Asn;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 98  
(D) OTHER INFORMATION: /note= "Xaa at position 98 is His,  
Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys,  
Arg, Tyr, or Pro;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site

(B) LOCATION: 99  
(D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile,  
Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 100  
(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys,  
Tyr, Leu, His, Arg, Ile, Ser, Gln, or ..."

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 101  
(D) OTHER INFORMATION: /note= "Xaa at position is Asp,  
Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile,  
Leu, or Gln;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 102  
(D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly,  
Leu, Glu, Lys, Ser, Tyr, or Pro;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 103  
(D) OTHER INFORMATION: /note= "Xaa at position 103 is Asp,  
or Ser;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 104  
(D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp,  
Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 105  
(D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn,  
Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 106  
(D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu,  
Ser, Ala, Lys, Thr, Ile, Gly, or Pro;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 108  
(D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg,  
Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 110

(D) OTHER INFORMATION: /note= "Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 111

(D) OTHER INFORMATION: /note= "Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 112

(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 113

(D) OTHER INFORMATION: /note= "Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 114

(D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 115

(D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 116

(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 117

(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 118

(D) OTHER INFORMATION: /note= "Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 119  
 (D) OTHER INFORMATION: /note= "Xaa at position 119 is Glu, Ser, Lys, Pro, leu, Thr, Tyr, or Arg;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 120  
 (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 121  
 (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 122  
 (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 123  
 (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			35				40					45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	50					55				60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75					80	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			85					90					95		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu
			115					120					125		

Ser Leu Ala Ile Phe  
130

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 332 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 112  
    (D) OTHER INFORMATION: /note= "position 112 is deleted or  
Leu, Ala, Val, Ile, Pro, Phe, Trp, or M..."

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 113  
    (D) OTHER INFORMATION: /note= "position 113 is deleted or  
Pro, Phe, Ala, Leu, Ile, Trp, or Met"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 114  
    (D) OTHER INFORMATION: /note= "position 114 is deleted or  
Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:  
    (A) NAME/KEY: Modified-site  
    (B) LOCATION: 115  
    (D) OTHER INFORMATION: /note= "position 115 is deleted or  
Gln, Gly, Ser, Thr, Tyr or Asn"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
1                    5                    10                    15

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
20                    25                    30

His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
35                    40                    45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
50                    55                    60

Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
65                    70                    75                    80

Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	85	90	95	
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Xaa	100	105	110	
Xaa	Xaa	Xaa	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	115	120	125	
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	130	135	140	
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	Ala	145	150	155	160
Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	Pro	Asn	165	170	175	
Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	180	185	190	
Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	195	200	205	
Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	210	215	220	
Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe	225	230	235	240
Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	Gly	245	250	255	
Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	260	265	270	
Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	275	280	285	
Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro	290	295	300	
Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn	Thr	305	310	315	320
Ser	Tyr	Thr	His	Ser	Gln	Asn	Leu	Ser	Gln	Glu	Gly					325	330		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GYSRN

5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /note= "where x=(glyglyglyglyser)n  
and where n is an interger"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Ala Ala  
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /note= "where Xaa  
=(glyglyglyglyser)n and where n is an integer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Ala Ala  
1

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "where xaa = (gly(n)ser)m and where n is an integer and m is an int..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Xaa Ala Ala  
1

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "where Xaa=(alaglyser)n and where n is an integer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Ala Ala  
1

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly  
1 5 10 15  
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser  
20 25 30  
Gly Gly Gly Ser  
35

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro  
1 5 10 15  
Ser Lys Glu Ser His Lys Ser Pro  
20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ile Glu Gly Arg Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn  
1 5 10 15  
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
20 25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gly Gly Ser  
1

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGTCCATGG CNTCNCCNGC NCCNCCTGCT TGTGCACTCC GAGTC

45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGCACGAAT TCCCTGACGC AGAGGGTGA

30

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGACAAGCTT ACCTGACGCA GAGGGTGGAC CCT

33

- (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTCGGCAA

10

- (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATGTTGCCG

10

- (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCGGCGG CAA

13

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATGTTGCCG CCG

13

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATTCGGCGG CAACGGCGGC AA

22

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATGTTGCCG CCGTTGCCGC CG

22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGATCCATGG AGGTTACCCC TTTGCCT

27

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCAAGCTT ATGGGCACTG GCTCAGTCT

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGATACATGT TGCCTACACC TGTCTG

27

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCAAGCTT AAGGGTGAAC CTCTGGGCA

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGATCCATGG TCCTGCTGCC TGCTGTG

27

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:



GATCAAGCTT AAGGTGTAGG CAAAGGGTG

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGATCCATGG CTGTGGACTT TAGCTTGGA

30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCAAGCTT AAGGCAGCAG GACAGGTGT

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGATCCATGG ACTTTAGCTT GGGAGAA

27

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCAAGCTT ACACAGCAGG CAGCAGGAC

29

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGATCCATGG GAGAATGGAA AACCCAG

27

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GATCAAGCTT ACAAGCTAAA GTCCACAGC

29

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGATCCATGG GACCCACTTG CCTCTCA

27

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCAAGCTT ACAGTTGTCC CCGTGCTGC

29

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGTCCATGG GAACCCAGCT TCCTCCA

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATCAAGCTT AAAGGAGGCT CTGCAGGGC

29

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGATCCATGG GCAGGACCAC AGCTCAC

27

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCAAGCTT ACTGTGGAGG AAGCTGGGTT

30

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGATCCATGG CTCACAAGGA TCCCAATGCC

30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCAAGCTT ATGTGGTCCT GCGCTGTGG

29

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGATCCATGG ATCCCAATGC CATCTTCCTG

30

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATCAAGCTT ACTTGTGAGC TGTGGTCCT

29

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGATCCATGG CCATCTTCCT GAGCTTCCAA

30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCAAGCTT AATTGGGATC CTTGTGAGCT GT

32

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AATTCCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT 60

ACGTAGAGGG CGGTGGAGGC TCC 83

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCGGGGAGCC TCCACCGCCC TCTACGTACT GTTGAGCCTG CGCGTTCTCC AAGGTTTTCA 60

GATAGAAGGT CAGTTTACGA CGG 83

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAAGTCTC TATAATGAT 59

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGATCATTAT AGAGCAGTTA GAGCCACCAC CCTGTTGTTC CTGCGCTTGC TCAAGG 56

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTTACCCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG CAGCGGCGGC 60

GGTTCTAACT GCTCTATAAT 80

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGATCATTAT AGAGCAGTTA GAACCGCCGC CGTGCCACC GCCAGAGCCA CCACCCTGTT 60

GTTCCCTGCGC TTGCTCAAGG 80

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCGACCAT GGCTCTGGAC CCGAACAACC

30

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTCGATTACG TACAAAGGTG CAGGTGGT

28

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCGACCAT GGCTAATGCA TCAGGTATTG AG

32

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTCGATTACG TATTCTAAGT TCTTGACA

28

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GATCGACCAT GGCTGCACCC TCTCGACATC CA

32

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCGATTACG TAGGCCGTGG CAGAGGGC

28

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCGACCAT GGCTGCAGGT GACTGGCAAG AA

32

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CTCGATTACG TACTTGATGA TGATTGGA

28

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GCTCTGAGAG CCGCCAGAGC CGCCAGAGGG CTGCGCAAGG TGGCGTAGAA CGCG

54

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAG

54

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGGCTGCGCA AGGTGGCG

18

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACACCATTGG GCCCTGCCAG C

21

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GATCGACCAT GGCTTACAAG CTGTGCCACC CC

32

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGATCGAAGC TTATTAGGTG GCACACAGCT TCTCCT

36

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GATCGACCAT GGCTCCCGAG TTGGGTCCCA CC

32

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CGATCGAAGC TTATTAGGAT ATCCCTTCCA GGGCCT

36

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATCGACCAT GGCTATGGCC CCTGCCCTGC AG

32

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGATCGAAGC TTATTATCCC AGTTCTTCCA TCTGCT

36

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GATCGACCAT GGCTACCCAG GGTGCCATGC CG

32

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGATCGAAGC TTATTAGGGC TGCAGGGCAG GGGCCA

36

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CGATCGAAGC TTATTAGGGC TGCAGGGCAG GGGCCA

36

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CGATCGAAGC TTATTAGGCG AAGCCGGCA TGGCAC

36

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTAGAGGGCG GTGGAGGCTC C

21

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCGGGGAGCC TCCACCGCCC TCTAC

25

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTACGCCA CCTTGCGCAG CCCGGCGGCG GCTCTGACAT GTCTACACCA TTG

53

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CAATGGTGTA GACATGTCAG AGCCGCCGCC GGGCTGCGCA AGGTGGCGTA GAA 53

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60  
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120  
CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180  
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT 240  
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300  
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360  
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420  
CATAAATCTC CAAACATGT 439

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT 60  
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCTG 120  
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA 180

CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA	240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC	300
CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT	360
CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT	420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGGG AATTC	465

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA	60
CTCCTTACACA GCAGACTGAG CCAGTGCCCA GAGGTTACAC CTTTGCCTAC ACCTG	120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA	180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA	240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC	300
CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT	360
CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT	420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGGG AATTTCGGCGG CAACATGGCG	480
TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA	540
CTCCTTACACA GCAGACTGAG CCAGTGCCCA GAGGTTACAC CTTTGCCTAC ACCTG	600
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA	660
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA	720
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC	780
CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGGGCAGGA CCACAGCTCA CAAGGATCCC	840
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT	900

GTAGGAGGGT CCACCCTCTG CGTCAGG

927

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT	60
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCTG	120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA	180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA	240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC	300
CTTGGGGCCC TGCAGAGCCT CTTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT	360
CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT	420
TTCTGATGC TTGTAGGAGG GTCCACCCTC TGCCTCAGGG AATTCGGCAA CATGGCGTCT	480
CCCCTCCGC CTGCTTGTGA CCTCCGAGTC CTCAGTAAAC TGCTTCGTGA CTCCCATGTC	540
CTTCACAGCA GACTGAGCCA GTGCCCAGAG GTTACCCCTT TGCCTACACC TGTCTGCTG	600
CCTGCTGTGG ACTTTAGCTT GGGAGAATGG AAAACCCAGA TGGAGGAGAC CAAGGCACAG	660
GACATTCTGG GAGCAGTGAC CCTTCTGCTG GAGGGAGTGA TGGCAGCACG GGGACAACCTG	720
GGACCCACTT GCCTCTCATC CCTCCTGGGG CAGCTTTCTG GACAGGTCCG TCTCCTCCTT	780
GGGGCCCTGC AGAGCCTCCT TGGAACCCAG CTTCTCCAC AGGGCAGGAC CACAGCTCAC	840
AAGGATCCCA ATGCCATCTT CTTGAGCTTC CAACACCTGC TCCGAGGAAA GGTGCGTTTC	900
CTGATGCTTG TAGGAGGGTC CACCCTCTGC GTCAGG	936

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA	60
CTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTG	120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCA	180
CAGGACATTC TGGGAGCAGT GACCCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGG	240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTC	300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAG	360
CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT	420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TCGTCAGGG AATTCGGCGG CAACATGGCG	480
TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA	540
CTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTG	600
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCA	660
CAGGACATTC TGGGAGCAGT GACCCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGG	720
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTC	780
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAG	840
CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT	900
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TCGTCAGG	939

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 948 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TCCCCAGCGC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT	60
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCCTG	120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA	180
CAGGACATTC TGGGAGCAGT GACCCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA	240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC	300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT	360
CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT	420
TTCTTGATGC TTGTAGGAGG GTCCACCCTC TCGGTCAGGG AATTCGGCGG CAACGGCGGC	480
AACATGGCGT CCCCAGCGCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT	540
GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTACCCC TTTGCCTACA	600
CCTGTCCTGC TGCCTGCTGT GGACTTTAGC TTGGGAGAAT GGAAAACCCA GATGGAGGAG	660
ACCAAGGCAC AGGACATTCT GGGAGCAGTG ACCCTTCTGC TGGAGGGAGT GATGGCAGCA	720
CGGGGACAAC TGGGACCCAC TTGCCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC	780
CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC CTTGGAACCC AGCTTCCTCC ACAGGGCAGG	840
ACCACAGCTC ACAAGGATCC CAATGCCATC TTCCTGAGCT TCCAACACCT GCTCCGAGGA	900
AAGGTGCGTT TCCTGATGCT TGTAGGAGGG TCCACCCTCT GCGTCAGG	948

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC	60
ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA	120
CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC	180
AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC	240

CTCTCGACAT CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAAGTAC	300
GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAAGTCTC	360
TATAATGATC GATGAAATTA TACATCACTT AAAGAGACCA CCTGCACCTT TGCTGGACCC	420
GAACAACCTC AATGACGAAG ACGTCTCTAT CCTGATGGAC CGAAACCTTC GACTTCCAAA	480
CCTGGAGAGC TTCGTAAGGG CTGTCAAGAA CTTAGAAAAT GCATCAGGTA TTGAGGCAAT	540
TCTTCGTAAT CTCCAACCAT GTCTGCCCTC TGCCACGGCC GCACCCTCTC GACATCCAAT	600
CATCATCAAG GCAGGTGACT GGCAAGAATT CCGGGAAAAA CTGACGTTCT ATCTGGTTAC	660
CCTTGAGCAA GCGCAGGAAC AACAGTAC	688

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC	60
ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA	120
CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC	180
AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC	240
CTCTCGACAT CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAAGTAC	300
GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG	360
CAGCGGCGGC GGTTCCTAAT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG	420
ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT	480
GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA	540
AAATGCATCA GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC	600
GGCCGCACCC TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA	660
AAAACTGACG TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT AC	712

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 975 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGGCTCTGG	ACCCGAACAA	CCTCAATGAC	GAAGACGTCT	CTATCCTGAT	GGACCGAAAC	60
CTTCGACTTC	CAAACCTGGA	GAGCTTCGTA	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	120
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	180
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG	240
TTCTATCTGG	TTACCCCTGA	GCAAGCGCAG	GAACAACAGG	GTGGTGGCTC	TAAC TGCTCT	300
ATAATGATCG	ATGAAATTAT	ACATCACTTA	AAGAGACCAC	CTGCACCTTT	GTACGTAGAG	360
GGCGGTGGAG	GCTCCCCGGG	TGAACCGTCT	GGTCCAATCT	CTACTATCAA	CCCGTCTCCT	420
CCGTCTAAAG	AATCTCATAA	ATCTCCAAAC	ATGGCTACCC	AGGGTGCCAT	GCCGGCCTTC	480
GCCTCTGCTT	TCCAGCGCCG	GGCAGGAGGG	GTCCTGGTTG	CTAGCCATCT	GCAGAGCTTC	540
CTGGAGGTGT	CGTACCGCGT	TCTACGCCAC	CTTGCGCAGC	CCTCTGGCGG	CTCTGGCGGC	600
TCTCAGAGCT	TCCTGTCTAA	GTCTTTAGAG	CAAGTGAGAA	AGATCCAGGG	CGATGGCGCA	660
GCGCTCCAGG	AGAAGCTGTG	TGCCACCTAC	AAGCTGTGCC	ACCCCGAGGA	GCTGGTGTCTG	720
CTCGGACACT	CTCTGGGCAT	CCCCTGGGCT	CCCCTGAGCT	CCTGCCCCAG	CCAGGCCCTG	780
CAGCTGGCAG	GCTGCTTGAG	CCAACTCCAT	AGCGGCCTTT	TCCTCTACCA	GGGGCTCCTG	840
CAGGCCCTGG	AAGGGATATC	CCCCGAGTTG	GGTCCCACCT	TGGACACACT	GCAGCTGGAC	900
GTCGCCGACT	TTGCCACCAC	CATCTGGCAG	CAGATGGAAG	AACTGGGAAT	GGCCCCTGCC	960
CTGCAGCCCT	AATAA					975

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 975 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGGCTCTGG	ACCCGAACAA	CCTCAATGAC	GAAGACGTCT	CTATCCTGAT	GGACCGAAAC	60
CTTCGACTTC	CAAACCTGGA	GAGCTTCGTA	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	120
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	180
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG	240
TTCTATCTGG	TTACCCCTGA	GCAAGCGCAG	GAACAACAGG	GTGGTGGCTC	TAACTGCTCT	300
ATAATGATCG	ATGAAATTAT	ACATCACTTA	AAGAGACCAC	CTGCACCTTT	GTACGTAGAG	360
GGCGGTGGAG	GCTCCCCGGG	TGAACCGTCT	GGTCCAATCT	CTACTATCAA	CCCGTCTCCT	420
CCGTCTAAAG	AATCTCATAA	ATCTCCAAAC	ATGGCTACCC	AGGGTGCCAT	GCCGGCCTTC	480
GCCTCTGCTT	TCCAGCGCCG	GGCAGGAGGG	GTCCTGGTTG	CTAGCCATCT	GCAGAGCTTC	540
CTGGAGGTGT	CGTACCGCGT	TCTACGCCAC	CTTGCGCAGC	CCTCTGGCGG	CTCTGGCGGC	600
TCTCAGAGCT	TCCTGCTCAA	GTCTTTAGAG	CAAGTGAGAA	AGATCCAGGG	CGATGGCGCA	660
GCGCTCCAGG	AGAAGCTGTG	TGCCACCTAC	AAGCTGTGCC	ACCCCGAGGA	GCTGGTGCTG	720
CTCGGACACT	CTCTGGGCAT	CCCCTGGGCT	CCCCTGAGCT	CCTGCCCCAG	CCAGGCCCTG	780
CAGCTGGCAG	GCTGCTTGAG	CCAACTCCAT	AGCGGCCTTT	TCCTCTACCA	GGGGCTCCTG	840
CAGGCCCTGG	AAGGGATATC	CCCCGAGTTG	GGTCCCACCT	TGGACACACT	GCAGCTGGAC	900
GTCGCCGACT	TTGCCACCAC	CATCTGGCAG	CAGATGGAAG	AACTGGGAAT	GGCCCCTGCC	960
CTGCAGCCCT	AATAA					975

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 975 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:



ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG	60
GAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC	120
TCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	180
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	240
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	300
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CTACGTAGAG	360
GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT	420
CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC	480
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC	540
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC	600
TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA	660
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG	720
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG	780
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG	840
CAGGCCCTGG AAGGGATATC CCCCAGATTG GGTCCCACCT TGGACACACT GCAGCTGGAC	900
GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCTGCC	960
CTGCAGCCCT AATAA	975

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGGCTGCAG GTGACTGGCA AGAATTCCGG GAAAACTGA CGTTCTATCT GGTTACCCTT	60
GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTAACTGCT CTATAATGAT CGATGAAATT	120
ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA	180

GACGTCTCTA TCCTGATGGA CCGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG	240
GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA	300
TGTCTGCCCT CTGCCACGGC CGCACCTCT CTGACATCCAA TCATCATCAA GTACGTAGAG	360
GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT	420
CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC	480
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC	540
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC	600
TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA	660
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCGAGGA GCTGGTGCTG	720
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG	780
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG	840
CAGGCCCTGG AAGGGATATC CCCCAGATTG GGTCCCACCT TGGACACACT GCAGCTGGAC	900
GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC	960
CTGCAGCCCT AATAA	975

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	60
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	120
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	180
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	240
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TGGCGGTGGC	300
AGCGGCGGCG GTTCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA	360
CCACCTGCAC CTTTGTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA	420

ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT	480
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG	540
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	600
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG	660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG	720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG	780
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC	840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCGA GTTGGGTCCC	900
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG	960
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA	999

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTGTAATC TCCAACCATG TCTGCCCTCT	60
GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG CAGGTGACTG GCAAGAATTC	120
CGGGAAAAAC TGACGTTCTA TCTGGTTACC CTTGAGCAAG CGCAGGAACA ACAGGGTGGT	180
GGCTCTGGCG GTGGCAGCGG CGGCGGTTCT AACTGCTCTA TAATGATCGA TGAAATTATA	240
CATCACTTAA AGAGACCACC TGCACCTTTG CTGGACCCGA ACAACCTCAA TGACGAAGAC	300
GTCTCTATCC TGATGGACCG AAACCTTCGA CTTCCAAACC TGGAGAGCTT CGTAAGGGCT	360
GTCAAGAACT TAGAATACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA	420
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT	480
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG	540
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	600

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG	660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG	720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG	780
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC	840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC	900
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG	960
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA	999

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG	60
GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC	120
TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC TGCTCTATAA TGATCGATGA AATTATACAT	180
CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC	240
TCTATCCTGA TGGACCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC	300
AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG	360
CCCTCTGCCA CGGCCTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA	420
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT	480
ACCCAGGGTG CCATGCCGGC CTTGCGCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG	540
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	600
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG	660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG	720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG	780

AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC	840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC	900
ACCTTGACACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG	960
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA	999

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGCTGCAG GTGACTGGCA AGAATTCGG GAAAACTGA CGTTCATCT GGTACCCCTT	60
GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC	120
TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC ACCTTTGCTG	180
GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA CCTTCGACTT	240
CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC AGGTATTGAG	300
GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC CTCTCGACAT	360
CCAATCATCA TCAAGTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA	420
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT	480
ACCCAGGGTG CCATGCCGGC CTTGCTCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG	540
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	600
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG	660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG	720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG	780
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC	840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC	900
ACCTTGACACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG	960

GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA

999

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT ACAAGCTGTG CCACCCGAG	420
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC	480
AGCCAGGCCC TGCGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC	540
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA	600
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA	660
ATGGCCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG	720
CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC	780
CGCGTTCTAC GCCACCTTGC GCAGCCCTCT GCGGCTCTG GCGGCTCTCA GAGCTTCCTG	840
CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG	900
CTGTGTGCCA CCTAATAA	918

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC	480
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG	540
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG	600
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	660
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG	720
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG	780
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC	840
CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG	900
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAA	960
TAA	963

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CCGAGTTGGG TCCCACCTTG	420
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA	480
CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT	540
TTCCAGCGCC GGGCAGGAGG GGTCTTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG	600
TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG GCTCTGGCGG CTCTCAGAGC	660
TTCTTGCTCA AGTCTTTAGA GCAAGTGAGA AAGATCCAGG GCGATGGCGC AGCGCTCCAG	720
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	780
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA	840
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	900
GAAGGGATAT CCTAATAA	918

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180



GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG	480
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT	540
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA	600
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA	660
CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GCGGCTCTC AGAGCTTCCT GCTCAAGTCT	720
TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC	780
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC	840
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA	900
CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCTAA	960
TAA	963

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA TGGCCCCTGC CCTGCAGCCC	420

ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG	480
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	540
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG	600
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG	660
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG	720
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC	780
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCGA GTTGGGTCCC	840
ACCTTGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG	900
GAAGAACTGG GATAATAA	918

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG	480
CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG	540
CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CTCTGGCGGC	600
TCTGGCGGCT CTCAGAGCTT CCTGCTCAAG TCTTTAGAGC AAGTGAGAAA GATCCAGGGC	660

GATGGCGCAG CGCTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCAGGAG	720
CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC	780
CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG	840
GGGCTCCTGC AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCACCTT GGACACACTG	900
CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGATAA	960
TAA	963

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CCCAGGGTGC CATGCCGGCC	420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC	480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTCTGG CGGCTCTGGC	540
GGCTCTCAGA GCTTCCTGCT CAAGTCTTTA GAGCAAGTGA GAAAGATCCA GGGCGATGGC	600
GCAGCGCTCC AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG	660
CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC	720
CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC	780
CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA CCTTGACAC ACTGCAGCTG	840
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT	900

GCCCTGCAGC CCTAATAA

918

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG	540
TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC	600
CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG	660
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT	720
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC	780
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA	840
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT	900
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA	960
TAA	963

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT CTGCTTTCCA GCGCCGGGCA	420
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA	480
CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GGCGGCTCTC AGAGCTTCCT GCTCAAGTCT	540
TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC	600
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GAACTCTCT GGGCATCCCC	660
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA	720
CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC	780
GAGTTGGGTC CCACCTTGGA CAACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC	840
TGGCAGCAGA TGGAAGAACT GGAATGGCC CCTGCCCTGC AGCCACCCA GGGTGCCATG	900
CCGGCCTTCG CCTAATAA	918

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 963 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTGGTT	480
GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG	540
CCCTCTGGCG GCTCTGGCGG CTCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA	600
AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC	660
CACCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC	720
TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT	780
TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC	840
TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA	900
GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTAA	960
TAA	963

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
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CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT ACAAGCTGTG CCACCCGAG	420
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC	480
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC	540
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA	600
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA	660
ATGGCCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG	720
CGCCGGGCAG GAGGGGTCCT GGTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC	780
CGCGTTCTAC GCCACCTTGC GCAGCCCACA CCATTGGGCC CTGCCAGCTC CCTGCCCCAG	840
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC	900
CAGGAGAAGC TGTGTGCCAC CTAATAA	927

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC	480
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG	540
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG	600
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	660
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG	720
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG	780
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC	840
CTTGCGCAGC CCACACCATT GGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG	900
TCTTTAGAGC AAGTGAGAAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT	960
GCCACCTAAT AA	972

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CCGAGTTGGG TCCCACCTTG	420
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA	480
CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT	540



TTCCAGCGCC GGGCAGGAGG GGTCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG	600
TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCACACCAT TGGGCCCTGC CAGCTCCCTG	660
CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA	720
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG	780
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG	840
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG	900
CAGGCCCTGG AAGGGATATC CTAATAA	927

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG	480
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT	540
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA	600
GGAGGGGTCC TGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA	660
CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG	720
CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG	780

CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG ACACTCTCTG	840
GGCATCCCCCT GGGCTCCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC	900
TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC CCTGGAAGGG	960
ATATCCTAAT AA	972

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA TGGCCCCTGC CCTGCAGCCC	420
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG	480
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	540
CAGCCCACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA	600
GAGCAAGTGA GAAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	660
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	720
GCTCCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	780
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCGAG	840
TTGGGTCCCA CCTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	900
CAGCAGATGG AAGAACTGGG ATAATAA	927

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 972 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG	480
CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG	540
CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CACACCATTG	600
GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG	660
ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC	720
CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC	780
TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC	840
CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG	900
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA	960
CTGGGATAAT AA	972

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 927 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CCCAGGGTGC CATGCCGGCC	420
TCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC	480
TCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCACACC ATTGGGCCCT	540
GCCAGCTCCC TGCCCCAGAG CTTCTGCTC AAGTCTTTAG AGCAAGTGAG AAAGATCCAG	600
GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCGAG	660
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC	720
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC	780
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA	840
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA	900
ATGGCCCCTG CCCTGCAGCC CTAATAA	927

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 972 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
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CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG	540
TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC	600
CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG	660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC	720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG	780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCTTTTCC TCTACCAGGG GCTCCTGCAG	840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG	960
CAGCCCTAAT AA	972

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT CTGCTTTCCA GCGCCGGGCA	420
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA	480
CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG	540
CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG	600
CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG AACTCTCTG	660
GGCATCCCCCT GGGCTCCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC	720
TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC CCTGGAAGGG	780
ATATCCCCCG AGTTGGGTCC CACCTTGGAC AACTGCAGC TGGACGTCGC CGACTTTGCC	840
ACCACCATCT GGCAGCAGAT GGAAGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCAG	900
GGTGCCATGC CGGCCTTCGC CTAATAA	927

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTTGTT	480
GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG	540

CCCACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG	600
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC	660
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT	720
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT	780
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCAGATTG	840
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG	900
CAGATGGAAG AACTGGGAAT GGCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC	960
TTCGCCTAAT AA	972

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTAAT GGACAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG	540
TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC	600
CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG	660
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT	720

CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC	780
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA	840
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT	900
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA	960
TAA	963

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG	540
TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTTG GCCCTGCCAG CTCCCTGCCC	600
CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG	660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC	720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG	780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCTTTTTC TCTACCAGGG GCTCCTGCAG	840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG	960



CAGCCCTAAT AA

972

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG	540
TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC	600
CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG	660
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT	720
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC	780
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA	840
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT	900
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA	960
TAA	963

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTAAT GGACAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG	540
TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC	600
CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG	660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC	720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG	780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG	840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	900
CCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG	960
CAGCCCTAAT AA	972

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 918 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA GGTTCACCTT TTGCCTACAC CTGTCCTGCT GCCTGCTGTG	480
GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA CCAAGGCACA GGACATTCTG	540
GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG ATGGCAGCAC GGGGACAACT GGGACCCACT	600
TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG	660
CAGAGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC	720
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT	780
GTAGGAGGGT CCACCTCTG CGTCAGGGAA TTCGGCGGCA ACATGGCGTC TCCCGCTCCG	840
CCTGCTTGTTG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC	900
AGACTGAGCC AGTGCCCA	918

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
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TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG	480
GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC	540
CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC	600
CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT	660
GGAACCCAGC TTCCTCCACA GGGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC	720
CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC	780
ACCCTCTGCG TCAGGGAATT CGGCGGCAAC ATGGCGTCTC CCGCTCCGCC TGCTTGTGAC	840
CTCCGAGTCC TCAGTAAACT GCTTCGTGAC TCCCATGTCC TTCACAGCAG ACTGAGCCAG	900
TGCCCAGAGG TTCACCT	918

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA	480
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG	540
GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG	600
CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT	660
CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA	720
CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC	780
AGGGAATTCG GCGGCAACAT GGCCTCTCCC GCTCCGCCTG CTTGTGACCT CCGAGTCCTC	840
AGTAAACTGC TTCGTGACTC CCATGTCCTT CACAGCAGAC TGAGCCAGTG CCCAGAGGTT	900
CACCCTTTGC CTACACCT	918

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG	480
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA	540
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG	600

GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC	660
AGGACCACAG CTCACAAGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA	720
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC	780
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT	840
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT	900
ACACCTGTCC TGCTGCCT	918

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	480
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	540
GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT	600
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	660
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG	720
TGCGTTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC	780
ATGGCGTCTC CCGCTCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC	840
TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCAGAGG TTCACCCTTT GCCTACACCT	900

GTCCTGCTGC CTGCTGTG

918

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCGGTTAC CCTTGAGCAA GCGCAGGAAC AACAGTACGT AGAGGGCGGT GGAGGCTCCC	360
CGGGGAACCG TCTGGTCCAA TCTCTACTAT CAACCCGTCT CCTCCGTCTA AAGAATCTCA	420
TAAACTCCAA ACATGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT	480
CTGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA	540
CTTGCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT	600
GCAGGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC	660
AATGCATCTT CCTGAGCTTC CAACACCTGC TCCGAGGAAA GGTGCGTTTC CTGATGCTTG	720
TAGGGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC ATGGCGTCTC CCGCTCCGCC	780
TGCTGTGACC TCCGAGTCCT CAGTAACTG CTTGCTGACT CCCATGTCCT TCACAGCAGA	840
CTGACCAGTG CCCAGAGGTT CACCCTTTGC CTACACCTGT CCTGCTGCCT GCTGTGGACT	900
TTAGTTG	907

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA	480
CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG	540
GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC	600
CGAGGAAAGG TGCGTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC	660
GGCGGCAACA TGGCGTCTCC CGCTCCGCCT GCTTGTGACC TCCGAGTCCT CAGTAAACTG	720
CTTCGTGACT CCCATGTCCT TCACAGCAGA CTGAGCCAGT GCCCAGAGGT TCACCCTTTG	780
CCTACACCTG TCCTGCTGCC TGCTGTGGAC TTTAGCTTGG GAGAATGGAA AACCCAGATG	840
GAGGAGACCA AGGCACAGGA CATTCTGGGA GCAGTGACCC TTCTGCTGGA GGGAGTGATG	900
GCAGCACGGG GACAACTG	918

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 848 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:



GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG AACCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG	480
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG	540
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCT GCGGCAACAT GCGTCTCCC	600
GCTCCGCCTG CTTGTGACCT CCGAGTCCTC AGTAACTGC TTCGTGACTC CCATGTCCTT	660
CACAGCAGAC TGAGCCAGTG CCCAGAGGTT CACCCTTTGC CTACACCTGT CCTGCTGCCT	720
GCTGTGGACT TTAGCTTGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC	780
ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA	840
CCCACTTG	848

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG	480
AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC	540
CTCTGCGTCA GGGGAATTCGG CGGCAACATG GCGTCTCCCG CTCCGCTGC TTGTGACCTC	600
CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC	660
CCAGAGGTTT ACCCTTTGCC TACACCTGTC CTGCTGCCTG CTGTGGACTT TAGCTTGGGA	720
GAATGGAAAA CCCAGATGGA GGAGACCAAG GCACAGGACA TTCTGGGAGC AGTGACCCTT	780
CTGCTGGAGG GAGTGATGGC AGCACGGGGA CAACTGGGAC CCACTTGCCT CTCATCCCTC	840
CTGGGGCAGC TTTCTGGACA GGTCCGTCTC CTCCTTGGGG CCCTGCAGAG CCTCCTTGA	900
ACCCAGCTTC CTCCACAG	918

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC	480
CTGCTCCGAG GAAAGGTGCG TTTCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG	540
GAATTCGGCG GCAACATGGC GTCTCCCGCT CCGCCTGCTT GTGACCTCCG AGTCCTCAGT	600

AAACTGCTTC GTGACTCCCA TGTCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC	660
CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC	720
CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA	780
GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT	840
TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT	900
CCACAGGGCA GGACCACA	918

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA TCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA	480
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC	540
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT	600
CGTGACTCCC ATGTCCCTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT	660
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG	720
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA	780
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG	840

GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGA CCCAGCTTCC TCCACAGGGC	900
AGGACCACAG CTCACAAG	918

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG	480
CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGGAATTCGG CGGCAACATG	540
GCGTCTCCCG CTCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC	600
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC	660
CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA CCCAGATGGA GGAGACCAAG	720
GCACAGGACA TTCTGGGAGC AGTGACCCTT CTGCTGGAGG GAGTGATGGC AGCACGGGGA	780
CAACTGGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA GGTCCGTCTC	840
CTCCTTGGGG CCCTGCAGAG CCTCCTTGGA ACCCAGCTTC CTCCACAGGG CAGGACCACA	900
GCTCACAAGG ATCCCAAT	918

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA GGTTCACCTT TTGCCTACAC CTGTCCTGCT GCCTGCTGTG	480
GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA CCAAGGCACA GGACATTCTG	540
GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG ATGGCAGCAC GGGGACAACT GGGACCCACT	600
TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG	660
CAGAGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC	720
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT	780
GTAGGAGGGT CCACCCTCTG CGTCAGGGAA TTCGGCAACA TGGCGTCTCC CGCTCCGCCT	840
GCTTGTGACC TCCGAGTCCT CAGTAAACTG CTTCTGTGACT CCCATGTCCT TCACAGCAGA	900
CTGAGCCAGT GCCCA	915

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 915 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG	480
GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC	540
CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC	600
CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT	660
GGAACCCAGC TTCCTCCACA GGGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC	720
CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC	780
ACCTCTGCG TCAGGGAATT CGGCAACATG GCGTCTCCCG CTCCGCCTGC TTGTGACCTC	840
CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC	900
CCAGAGGTTC ACCCT	915

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA	480
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG	540
GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG	600
CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT	660
CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA	720
CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC	780
AGGGAATTCG GCAACATGGC GTCTCCCGCT CCGCCTGCTT GTGACCTCCG AGTCCTCAGT	840
AAACTGCTTC GTGACTCCCA TGTCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC	900
CCTTTGCCTA CACCT	915

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420

CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG	480
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA	540
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG	600
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGA CCCAGCTTCC TCCACAGGGC	660
AGGACCACAG CTCACAAGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA	720
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC	780
AACATGGCGT CTCCCGCTCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT	840
GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTCACCC TTTGCCTACA	900
CCTGTCTGCTG TGCCT	915

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	480
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	540
GGACAACCTG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT	600
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	660
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG	720



GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCAACATG	780
GCGTCTCCCG CTCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC	840
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC	900
CTGCTGCCTG CTGTG	915

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC	480
ATTCTGGGAG CAGTGACCCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA	540
CCCACTTGCC TCTCATCCCT CCTGGGGCAG CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG	600
GCCCTGCAGA GCCTCCTTGG AACCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG	660
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG	720
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCAACATGGC GTCTCCCGCT	780
CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AAACTGCTTC GTGACTCCCA TGTCTTCAC	840
AGCAGACTGA GCCAGTGCCC AGAGGTTTAC CCTTTGCCTA CACCTGTCCT GCTGCCTGCT	900
GTGGACTTTA GCTTG	915

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA	480
CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG	540
GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC	600
CGAGGAAAGG TCGTTTTCTT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC	660
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT	720
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT	780
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG	840
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA	900
GCACGGGGAC AACTG	915

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG AAGCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG	480
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG	540
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCAACATGGC GTCTCCCGCT	600
CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AACTGCTTC GTGACTCCCA TGTCTTCAC	660
AGCAGACTGA GCCAGTGCCC AGAGGTTTAC CCTTTGCCTA CACCTGTCCT GCTGCCTGCT	720
GTGGACTTTA GCTTGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT	780
CTGGGAGCAG TGACCTTCT GCTGGAGGGA GTGATGGCAG CACGGGGACA ACTGGGACCC	840
ACTTGCTCT CATCCCTCCT GGGGAGCTT TCTGGACAGG TCCGTCTCCT CTTGGGGCC	900
CTGCAGAGCC TCCTT	915

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
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TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG	480
AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC	540
CTCTGCGTCA GGAATTCGG CAACATGGCG TCTCCCGCTC CGCCTGCTTG TGACCTCCGA	600
GTCCTCAGTA AACTGCTTCG TGA TCTCCAT GTCCTTCACA GCAGACTGAG CCAGTGCCCA	660
GAGGTTCAAC CTTTGCCTAC ACCTGTCCTG CTGCCTGCTG TGGACTTTAG CTTGGGAGAA	720
TGGA AAAACC AGATGGAGGA GACCAAGGCA CAGGACATTC TGGGAGCAGT GACCCCTCTG	780
CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA CTTGCCTCTC ATCCCTCCTG	840
GGGCAGCTTT CTGGACAGGT CCGTCTCCTC CTTGGGGCCC TGCAGAGCCT CCTTGGAACC	900
CAGCTTCCTC CACAG	915

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC	480
CTGCTCCGAG GAAAGGTGCG TTTCTTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG	540
GAATTCGGCA ACATGGCGTC TCCCGCTCCG CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA	600
CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGAGCC AGTGCCGAGA GGTTCACCCT	660
TTGCCTACAC CTGTCCTGCT GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG	720
ATGGAGGAGA CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG	780
ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT	840
GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC TTGGAACCCA GCTTCCTCCA	900
CAGGGCAGGA CCACA	915

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA	480
GGAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC	540
AACATGGCGT CTCCCGCTCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT	600

GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTACACC TTTGCCTACA	660
CCTGTCTCTGC TGCCTGCTGT GGACTTTAGC TTGGGAGAAT GGAAAACCCA GATGGAGGAG	720
ACCAAGGCAC AGGACATTCT GGGAGCAGTG ACCCTTCTGC TGGAGGGAGT GATGGCAGCA	780
CGGGGACAAC TGGGACCCAC TTGCCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC	840
CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC CTTGGAACCC AGCTTCCTCC ACAGGGCAGG	900
ACCACAGCTC ACAAG	915

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG	480
CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGGAATTCGG CAACATGGCG	540
TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA TCTCCAT	600
GTCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCTG	660
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA	720
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA	780
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC	840
CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGCAG GACCACAGCT	900

CACAAGGATC CCAAT

915

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
GACTTCCAAA CCTGGAGAGC TTCGTAAGGG CTGTCAAGAA CTTAGAAAAT GCATCAGGTA	180
TGAGGCAATT CTTCGTAATC TCCAACCATG TCTGCCCTCT GCCACGGCCG CACCCTCTCG	240
CATCCAATCA TCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT	300
TGTTTACCCT TGAGCAAGCG CAGGAACAAC AGTACGTAGA GGGCGGTGGA GGCTCCCCGG	360
TAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA	420
TCTCCAAACA TGGAGGTTCA CCCTTTGCCT ACACCTGTCC TGCTGCCTGC TGTGGACTTT	480
AGCTTGGGAG AATGGAAAAAC CCAGATGGAG GAGACCAAGG CACAGGACAT TCTGGGAGCA	540
GTGACCCTTC TGCTGGAGGG AGTGATGGCA GCACGGGGAC AACTGGGACC CACTTGCCTC	600
TCATCCCTCC TGGGGCAGCT TTCTGGACAG GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC	660
CTCCTTGGA CCCAGCTTCC TCCACAGGGC AGGACCACAG CTCACAAGGA TCCCAATGCC	720
ATCTTCCTGA GCTTCCAACA CCTGCTCCGA GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA	780
GGGTCCACCC TCTGCGTCAG GGAATTCGGC GGCAACGGCG GCAACATGGC GTCCCCAGCG	840
CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AACTGCTTC GTGACTCCCA TGTCTTCAC	900
AGCAGACTGA GCCAGTGCCC A	921

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG	480
GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC	540
CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC	600
CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT	660
GGAACCCAGC TTCCTCCACA GGGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC	720
CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC	780
ACCCTCTGCG TCAGGGAATT CGGCGGCAAC GGCGGCAACA TGGCGTCCCC AGCGCCGCCT	840
GCTTGTGACC TCCGAGTCCT CAGTAAACTG CTTCGTGACT CCCATGTCCT TCACAGCAGA	900
CTGAGCCAGT GCCCAGAGGT TCACCCCT	927

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA	480
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG	540
GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG	600
CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT	660
CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA	720
CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC	780
AGGGAATTCG GCGGCAACGG CGGCAACATG GCGTCCCCAG CGCCGCCTGC TTGTGACCTC	840
CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC	900
CCAGAGGTTC ACCCTTTGCC TACACCT	927

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG	480
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA	540
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG	600
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGA CCCAGCTTCC TCCACAGGGC	660
AGGACCACAG CTCACAAGGA TCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA	720
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC	780
GGCAACGGCG GCAACATGGC GTCCCCAGCG CCGCCTGCTT GTGACCTCCG AGTCCTCAGT	840
AAACTGCTTC GTGACTCCCA TGTCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC	900
CCTTTGCCTA CACCTGTCCT GCTGCCT	927

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	480

AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	540
GGACAACCTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT	600
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	660
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG	720
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC	780
GGCGGCAACA TGGCGTCCCC AGCGCCGCTT GCTTGTGACC TCCGAGTCCT CAGTAAACTG	840
CTTCGTGACT CCCATGTCCT TCACAGCAGA CTGAGCCAGT GCCCAGAGGT TCACCCTTTG	900
CCTACACCTG TCCTGCTGCC TGCTGTG	927

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC	480
ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA	540
CCCACTTGCC TCTCATCCCT CCTGGGGCAG CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG	600
GCCCTGCAGA GCCTCCTTGG AACCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG	660
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG	720
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGCAACGG CGGCAACATG	780

GCGTCCCCAG CGCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC	840
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC	900
CTGCTGCCTG CTGTGGACTT TAGCTTG	927

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA	480
CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG	540
GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC	600
CGAGGAAAGG TGCCTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC	660
GGCGGCAACG GCGGCAACAT GGCGTCCCCA GCGCCGCCTG CTTGTGACCT CCGAGTCCTC	720
AGTAAACTGC TTCGTGACTC CCATGTCCTT CACAGCAGAC TGAGCCAGTG CCCAGAGGTT	780
CACCCTTTGC CTACACCTGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA	840
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG	900
GGAGTGATGG CAGCACGGGG ACAACTG	927

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 927 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG AACCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG	480
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG	540
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGGCAACGG CGGCAACATG	600
GCGTCCCCAG CGCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC	660
CATGTCTTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC	720
CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA CCCAGATGGA GGAGACCAAG	780
GCACAGGACA TTCTGGGAGC AGTGACCCTT CTGCTGGAGG GAGTGATGGC AGCACGGGGA	840
CAACTGGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA GGTCCGTCTC	900
CTCCTTGGGG CCCTGCAGAG CCTCCTT	927

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 927 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG	480
AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC	540
CTCTGCGTCA GGAATTCGG CGGCAACGGC GGCAACATGG CGTCCCCAGC GCCGCCTGCT	600
TGTGACCTCC GAGTCCTCAG TAAACTGCTT CGTGACTCCC ATGTCCTTCA CAGCAGACTG	660
AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT ACACCTGTCC TGCTGCCTGC TGTGGACTTT	720
AGCTTGGGAG AATGGAAAAC CCAGATGGAG GAGACCAAGG CACAGGACAT TCTGGGAGCA	780
GTGACCCCTT TGCTGGAGGG AGTGATGGCA GCACGGGGAC AACTGGGACC CACTTGCCCTC	840
TCATCCCTCC TGGGGCAGCT TTCTGGACAG GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC	900
CTCCTTGGA CCCAGCTTCC TCCACAG	927

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC	480
CTGCTCCGAG GAAAGGTGCG TTTCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG	540
GAATTCGGCG GCAACGGCGG CAACATGGCG TCCCCAGCGC CGCCTGCTTG TGACCTCCGA	600
GTCTCAGTA AACTGCTTCG TGAATCCCAT GTCCTTCACA GCAGACTGAG CCAGTGCCCA	660
GAGGTTCAAC CTTTGCCTAC ACCTGTCCTG CTGCCTGCTG TGGACTTTAG CTTGGGAGAA	720
TGGAACACCC AGATGGAGGA GACCAAGGCA CAGGACATTC TGGGAGCAGT GACCCTTCTG	780
CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA CTTGCTCTC ATCCCTCCTG	840
GGGCAGCTTT CTGGACAGGT CCGTCTCCTC CTTGGGGCCC TGCAGAGCCT CCTTGGAACC	900
CAGCTTCCTC CACAGGGCAG GACCACA	927

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420

CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA	480
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC	540
GGCAACGGCG GCAACATGGC GTCCCCAGCG CCGCCTGCTT GTGACCTCCG AGTCCTCAGT	600
AAACTGCTTC GTGACTCCCA TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC	660
CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC	720
CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA	780
GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT	840
TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT	900
CCACAGGGCA GGACCACAGC TCACAAG	927

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG	480
CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGAATTCGG CGGCAACGGC	540
GGCAACATGG CGTCCCCAGC GCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT	600
CGTGACTCCC ATGTCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT	660



ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG	720
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA	780
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG	840
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC	900
AGGACCACAG CTCACAAGGA TCCCAAT	927

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT	60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT	120
CGACTTCCAA ACCTGGAGAG CTTCTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT	180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT	240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC	300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC	360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT	420
CATAAATCTC CAAACATGGA TCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA	480
GGAAAGGTGC GTTTCCTGAT GCTTGTAAGG GGGTCCACCC TCTGCGTCAG GGAATTCGGC	540
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT	600
CGTGACTCCC ATGTCTTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT	660
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG	720
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA	780
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG	840
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGGGCAG GACCACAGCT	900

## (2) INFORMATION FOR SEQ ID NO:155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GTCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC	480
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG	540
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG	600
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	660
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG	720
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG	780
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC	840
CTTGCGCAGC CCGGCGGCGG CTCTGACATG GCTACACCAT TAGGCCCTGC CAGCTCCCTG	900
CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGGA AGATCCAGGG CGATGGCGCA	960
GCGCTCCAGG AGAAGCTGTG TGCCACCTAA TAA	993

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GTCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG	480
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT	540
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA	600
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA	660
CGCCACCTTG CGCAGCCCGG CGGCGGCTCT GACATGGCTA CACCATTAGG CCCTGCCAGC	720
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	780
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	840
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	900
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG	960
CTCCTGCAGG CCCTGGAAGG GATATCCTAA TAA	993

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 993 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GTCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTGGTT	480
GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG	540
CCCGGCGGCG GCTCTGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCAGAGC	600
TTCTTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	660
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	720
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA	780
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	840
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	900
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC	960
ACCCAGGGTG CCATGCCGGC CTTGCCTAA TAA	993

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
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CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GTCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG	480
CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG	540
CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CGGCGGCGGC	600
TCTGACATGG CTACACCAT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG	660
TCTTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT	720
GCCACCTACA AGCTGTGCCA CCCCAGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC	780
CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC	840
CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC	900
CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT TGCCACCACC	960
ATCTGGCAGC AGATGGAAGA ACTGGGATAA TAA	993

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300

TTCTATCTGG TTACCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GTCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG	540
TACCGCGTTC TACGCCACCT TGCGCAGCCC GCGGCGGGCT CTGACATGGC TACACCATTA	600
GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG	660
ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC	720
CCCAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC	780
TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC	840
CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG	900
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA	960
CTGGGAATGG CCCCTGCCCT GCAGCCCTAA TAA	993

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480

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AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGG CGGCGGCTCT      540
GACATGGCTA CACCATTGGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT      600
TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC      660
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC      720
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA      780
CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC      840
GAGTTGGGTC CCACCTTGGA CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC      900
TGGCAGCAGA TGGAAGAACT GGAATGGCC CCTGCCCTGC AGCCCACCCA TCCTGGTTGC      960
TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACGCGGTT CTACGCCACC TTGCGCAGCC     1020
CTGATAA                                           1027

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(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 155 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
1           5           10           15
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
20          25          30
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
35          40          45
Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
50          55          60
Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
65          70          75          80
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
85          90          95
Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
100         105         110
Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe

```

115		120		125
Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu				
130		135		140
Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe				
145		150		155

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu			
1	5	10	15
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val			
20	25	30	
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu			
35	40	45	
Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu			
50	55	60	
Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln			
65	70	75	80
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln			
85	90	95	
Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu			
100	105	110	
Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe			
115	120	125	
Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu			
130	135	140	
Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Met Ala			
145	150	155	160
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu			
165	170	175	
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val			



180	185	190
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu		
195	200	205
Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu		
210	215	220
Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln		
225	230	235
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln		
245	250	255
Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Gly		
260	265	270
Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln		
275	280	285
His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser		
290	295	300
Thr Leu Cys Val Arg		
305		

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu		
1	5	10
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val		
20	25	30
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu		
35	40	45
Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu		
50	55	60
Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln		
65	70	75
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln		

85					90					95					
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu
			100					105						110	
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe
		115					120					125			
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu
	130					135					140				
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Asn	Met	Ala	Ser
145					150					155					160
Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg
				165					170					175	
Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His
			180					185					190		
Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly
		195					200					205			
Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly
	210					215					220				
Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu
225					230					235					240
Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val
			245						250					255	
Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro
			260					265					270		
Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu
		275					280					285			
Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val
	290					295					300				
Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg								
305					310										

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 313 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	
1				5					10					15		
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	
			20					25					30			
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	
		35					40					45				
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	
	50					55					60					
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	
65					70					75					80	
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	
				85					90					95		
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	
			100					105						110		
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	
		115					120					125				
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	
	130					135					140					
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn	Met	Ala	
145					150					155					160	
Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	
				165					170					175		
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	
			180					185					190			
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	
		195					200					205				
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	
	210					215					220					
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	
225					230					235					240	
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	
				245					250					255		
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	
			260					265						270		
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	
		275					280					285				
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	

290

295

300

Val Gly Gly Ser Thr Leu Cys Val Arg  
305 310

## (2) INFORMATION FOR SEQ ID NO:165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	1	5	10	15
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	20	25	30	
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	35	40	45	
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	50	55	60	
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	65	70	75	80
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	85	90	95	
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	100	105	110	
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	115	120	125	
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	130	135	140	
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn	Gly	Gly	145	150	155	160
Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	165	170	175	
Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	180	185	190	
Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp				

195		200		205											
Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln
210						215						220			
Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala
225					230					235					240
Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu
				245					250					255	
Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly
			260					265					270		
Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn
		275					280					285			
Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe
	290					295					300				
Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg				
305					310					315					

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 302 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5				10					15		
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser
			20					25					30		
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35				40						45			
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
			85						90					95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr

100								105				110				
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
		115					120					125				
Asn	Met	Ala	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	
	130					135					140					
His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	
145					150					155					160	
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	
				165					170					175		
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	
		180						185					190			
Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	
		195					200					205				
Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	
	210					215					220					
Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	
225					230					235					240	
Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	
				245					250					255		
Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	
		260						265					270			
Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	
		275					280					285				
Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr			
	290					295					300					

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5				10					15		
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser

20					25					30					
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35					40					45			
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr
			100					105					110		
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser
		115					120					125			
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn
	130					135					140				
Met	Ala	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His
145					150					155					160
Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala
				165					170					175	
Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu
			180					185					190		
Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly
		195					200					205			
Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr
	210					215					220				
Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro
225					230					235					240
Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala
			245						250				255		
Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser
		260						265					270		
Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	Gly
		275					280					285			
Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln
	290					295					300				
Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr			
305					310					315					

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	1	5	10	15
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	20	25	30	
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	35	40	45	
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	50	55	60	
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	65	70	75	80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	100	105	110	
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	115	120	125	
Asn	Met	Ala	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	130	135	140	
Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	145	150	155	160
Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	165	170	175	
Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	180	185	190	
Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	195	200	205	
Pro	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	210	215	220	



Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	225	230	235	240
Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	245	250	255	
Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	260	265	270	
Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	275	280	285	
Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser			290	295	300	

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	1	5	10	15
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	20	25	30	
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	35	40	45	
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	50	55	60	
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	65	70	75	80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	100	105	110	
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	115	120	125	
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	130	135	140	

Met	Ala	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	145	150	155	160
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	165	170	175	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	180	185	190	
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	195	200	205	
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	210	215	220	
Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	225	230	235	240
Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	245	250	255	
Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	260	265	270	
His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	275	280	285	
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	290	295	300	
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser				305	310	315	

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	1	5	10	15
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	20	25	30	
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	35	40	45	

Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	50	55	60	
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	65	70	75	80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	100	105	110	
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	115	120	125	
Asn	Met	Ala	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	130	135	140	
Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	145	150	155	160
Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	165	170	175	
Leu	Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	180	185	190	
Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	195	200	205	
Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	210	215	220	
Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	225	230	235	240
Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	245	250	255	
Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	260	265	270	
Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	275	280	285	
Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	290	295	300			

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	
1				5					10					15		
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	
			20					25					30			
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	
		35					40					45				
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	
	50					55					60					
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	
65					70					75					80	
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	
				85					90					95		
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	
			100					105					110			
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	
		115					120					125				
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	
	130					135					140					
Met	Ala	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	
145					150					155					160	
Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	
				165					170					175		
His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	
			180					185					190			
Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	
		195					200					205				
Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	
	210					215					220					
Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	
225					230					235					240	
Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	
				245					250					255		
Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	
			260					265					270			

Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser
	275						280					285			
Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp
	290					295					300				
Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly			
305					310					315					

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 302 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5				10					15		
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser
			20				25					30			
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35				40					45				
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50				55					60					
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65				70				75						80	
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
			85					90						95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr
		100					105					110			
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser
	115					120					125				
Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln
	130				135					140					
Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu
145					150					155					160
Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly	Gly
				165				170						175	

Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg		
			180					185					190				
Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr		
		195					200					205					
Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu		
	210					215					220						
Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln		
225					230					235					240		
Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln		
			245						250					255			
Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr		
		260						265					270				
Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp		
	275						280					285					
Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro				
290						295					300						

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro		
1				5				10					15				
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser		
		20					25					30					
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val		
	35				40						45						
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu		
50					55					60							
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg		
65				70					75					80			
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys		
			85				90							95			

Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Tyr		
			100							105				110		
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	
			115							120				125		
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	
			130							135				140		
Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	
			145							150				155		
Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	
			165							170				175		
Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly	Gly	Ser	
			180							185				190		
Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	
			195							200				205		
Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	
			210							215				220		
Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	
			225							230				235		
Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	
			245							250				255		
Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	
			260							265				270		
Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	
			275							280				285		
Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	
			290							295				300		
Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro				
			305							310				315		

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro		
1				5					10					15			
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser		
			20					25					30				
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val		
		35					40					45					
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu		
	50					55					60						
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg		
65					70					75					80		
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys		
				85					90					95			
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr		
			100					105						110			
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser		
		115					120					125					
Asn	Met	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala		
	130					135					140						
Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His		
145					150					155					160		
Leu	Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu		
				165					170					175			
Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu		
		180					185						190				
Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu		
		195					200					205					
Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser		
	210					215					220						
Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His		
225					230				235						240		
Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile		
			245					250						255			
Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala		
		260						265					270				
Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala		
		275					280					285					
Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala				
	290					295					300						



(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	
1				5				10					15			
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	
			20				25					30				
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	
		35				40					45					
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	
		50			55					60						
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	
65				70				75					80			
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	
			85				90						95			
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	
		100					105					110				
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	
		115					120					125				
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	
		130				135					140					
Met	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	
145				150					155					160		
His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	
			165					170					175			
Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	
		180					185						190			
Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	
		195				200					205					
Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	
	210					215					220					

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
 225 230 235 240  
 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
 245 250 255  
 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 260 265 270  
 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
 275 280 285  
 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
 290 295 300  
 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
 1 5 10 15  
 Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser  
 20 25 30  
 Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val  
 35 40 45  
 Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu  
 50 55 60  
 Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg  
 65 70 75 80  
 His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys  
 85 90 95  
 Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr  
 100 105 110  
 Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser  
 115 120 125

Asn	Met	Ala	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly
130						135					140				
His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln
145					150					155					160
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe
				165					170					175	
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu
			180					185					190		
Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr
		195					200					205			
Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln
210						215					220				
Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg
225					230					235					240
Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val
				245					250					255	
Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Thr	Pro	Leu	Gly	Pro
			260					265					270		
Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val
		275					280					285			
Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala
290						295					300				
Thr															
305															

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 320 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5					10					15	
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser
			20					25					30		

Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35					40					45			
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
				85				90						95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr
			100					105					110		
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser
		115					120					125			
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn
	130					135					140				
Met	Ala	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His
145					150					155					160
Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala
				165					170					175	
Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu
			180					185					190		
Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly
	195						200					205			
Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr
	210					215					220				
Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro
225					230					235					240
Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala
				245					250					255	
Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser
			260					265					270		
Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Thr	Pro	Leu	Gly	Pro	Ala
	275						280					285			
Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg
	290					295					300				
Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 305 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	
1				5				10					15			
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	
			20				25					30				
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	
		35				40					45					
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	
	50				55				60							
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	
65			70					75					80			
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	
			85				90					95				
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	
		100					105					110				
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
	115					120					125					
Asn	Met	Ala	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	
	130				135				140							
Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	
145			150					155						160		
Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	
			165				170					175				
Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	
		180					185					190				
Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	
	195				200						205					
Pro	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	
	210				215					220						
Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	

225		230		235		240									
Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu
				245					250					255	
Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser
			260					265						270	
Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His
		275					280					285			
Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile
	290					295					300				
Ser															
305															

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 320 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5					10					15	
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser
			20					25					30		
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35				40						45			
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50				55						60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65				70					75					80	
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
			85					90						95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr
		100					105						110		
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser
		115					120					125			
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn

130		135		140											
Met	Ala	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val
145					150					155					160
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met
				165					170					175	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser
			180					185					190		
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln
	195					200						205			
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro
210						215					220				
Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys
225				230						235					240
Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln
				245					250					255	
Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val
		260						265					270		
Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys
	275						280					285			
Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser
	290					295					300				
Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5					10					15	
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser
			20					25					30		





(A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	1	5	10	15
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	20	25	30	
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	35	40	45	
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	50	55	60	
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	65	70	75	80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	100	105	110	
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	115	120	125	
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	130	135	140	
Met	Ala	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	145	150	155	160
Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	165	170	175	
His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	180	185	190	
Ala	Gln	Pro	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	195	200	205	
Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	210	215	220	
Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	225	230	235	240



Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu
145					150					155					160
Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Thr	Pro	Leu
			165						170					175	
Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu
			180					185					190		
Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu
		195					200					205			
Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly
	210					215					220				
His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln
225					230					235					240
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe
				245					250					255	
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu
			260					265						270	
Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr
		275					280					285			
Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln
	290					295					300				
Pro															
305															

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5					10					15	
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser
			20					25					30		
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35					40					45			

Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	50	55	60	
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	65	70	75	80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	100	105	110	
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	115	120	125	
Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	130	135	140	
Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	145	150	155	160
Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	165	170	175	
Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Thr	Pro	Leu	Gly	180	185	190	
Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	195	200	205	
Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	210	215	220	
Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	225	230	235	240
Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	245	250	255	
Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	260	265	270	
Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	275	280	285	
Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	290	295	300	
Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	305	310	315	320

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	
1				5				10						15		
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	
			20				25						30			
Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	
		35				40						45				
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	
	50					55					60					
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	
65					70				75						80	
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	
				85				90						95		
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Tyr	
			100					105					110			
Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
		115					120					125				
Asn	Met	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	
	130					135					140					
Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	
145					150					155					160	
Leu	Ala	Gln	Pro	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	
				165					170					175		
Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	
			180					185					190			
Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	
		195					200					205				
Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	
	210					215					220					
Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	
225					230					235					240	
Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	

	245		250		255
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu					
	260		265		270
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu					
	275		280		285
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe					
	290		295		300
Ala					
305					

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro					
1	5		10		15
Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser					
	20		25		30
Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val					
	35		40		45
Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu					
	50		55		60
Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg					
	65		70		75
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys					
	85		90		95
Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr					
	100		105		110
Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser					
	115		120		125
Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn					
	130		135		140
Met Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser					

145		150		155		160									
His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu
				165					170					175	
Ala	Gln	Pro	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe
			180					185					190		
Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala
		195					200					205			
Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu
	210					215					220				
Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu
225					230					235					240
Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln
				245					250					255	
Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu
			260					265					270		
Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp
		275					280					285			
Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly
	290					295					300				
Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	Ile	Leu	Met	Asp
1				5				10					15		
Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	Ala	Val	Lys
		20					25					30			
Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn	Leu	Gln
	35					40					45				

Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro	Ile	Ile	50	55	60
Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	65	70	75
Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Gly	Gly	Gly	Ser	Asn	85	90	95
Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	Pro	100	105	110
Ala	Pro	Leu	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	115	120	125
Gly	Pro	Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	130	135	140
Lys	Ser	Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	145	150	155
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	165	170	175
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	180	185	190
Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	195	200	205
Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	210	215	220
Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	225	230	235
His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	245	250	255
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	260	265	270
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	275	280	285
Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	290	295	300
Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	305	310	315
Pro																		

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 321 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	1	5	10	15
Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	20	25	30	
Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	35	40	45	
Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Gly	Gly	Gly	Ser	Asn	Cys	Ser	Ile	50	55	60	
Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	Pro	Ala	Pro	Leu	65	70	75	80
Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	Ile	Leu	Met	Asp	85	90	95	
Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	Ala	Val	Lys	100	105	110	
Asn	Leu	Glu	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	115	120	125	
Gly	Pro	Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	130	135	140	
Lys	Ser	Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	145	150	155	160
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	165	170	175	
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	180	185	190	
Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	195	200	205	
Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	210	215	220	
Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	225	230	235	240

His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln
				245					250					255	
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe
			260					265					270		
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu
		275					280					285			
Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr
	290					295					300				
Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln
305					310					315					320
Pro															

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Ala	Pro	Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu
1				5					10					15	
Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln
			20					25					30		
Glu	Gln	Gln	Gly	Gly	Gly	Ser	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile
		35					40					45			
Ile	His	His	Leu	Lys	Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn
	50					55					60				
Leu	Asn	Asp	Glu	Asp	Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu
65					70					75				80	
Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala
				85				90						95	
Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser
		100						105					110		
Ala	Thr	Ala	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser
		115					120					125			

Gly	Pro	Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	130	135	140	
Lys	Ser	Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	145	150	155	160
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	165	170	175	
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	180	185	190	
Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	195	200	205	
Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	210	215	220	
Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	225	230	235	240
His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	245	250	255	
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	260	265	270	
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	275	280	285	
Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	290	295	300	
Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	305	310	315	320
Pro																			

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val
1				5					10					15	

Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Gly	Gly	Gly	Ser	Asn	Cys	Ser
			20					25					30		
Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	Pro	Ala	Pro
		35					40					45			
Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	Ile	Leu	Met
	50					55					60				
Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	Ala	Val
65					70					75					80
Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn	Leu
				85					90					95	
Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro	Ile
			100					105					110		
Ile	Ile	Lys	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser
		115					120					125			
Gly	Pro	Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His
	130					135					140				
Lys	Ser	Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser
145					150				155						160
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln
				165				170						175	
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro
			180					185					190		
Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu
		195					200					205			
Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu
	210					215					220				
Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly
225					230					235					240
His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln
				245					250					255	
Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe
			260					265					270		
Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu
		275					280					285			
Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr
	290					295					300				
Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln

305	310	315	320
Pro			

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	Ile	Leu	Met	Asp	1	5	10	15
Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	Ala	Val	Lys	20	25	30	
Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn	Leu	Gln	35	40	45	
Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro	Ile	Ile	50	55	60	
Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	65	70	75	80
Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	Gly	Gly	Gly	Ser	Gly	85	90	95	
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	100	105	110	
Ile	His	His	Leu	Lys	Arg	Pro	Pro	Ala	Pro	Leu	Tyr	Val	Glu	Gly	Gly	115	120	125	
Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	Thr	Ile	Asn	Pro	130	135	140	
Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	Met	Ala	Thr	Gln	145	150	155	160
Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	165	170	175	
Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	180	185	190	
Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln				

195		200		205
Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp				
210		215		220
Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His				
225		230		240
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala				
	245		250	255
Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu				
	260		265	270
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala				
	275		280	285
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln				
	290		295	300
Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu				
305		310		320
Leu Gly Met Ala Pro Ala Leu Gln Pro				
	325			

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu				
1	5	10	15	
Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala				
	20	25	30	
Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr				
	35	40	45	
Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser Gly Gly Gly Ser				
	50	55	60	
Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His				
65	70	75	80	
Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp				



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Ala	Pro	Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	
1				5					10					15		
Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	
			20					25					30			
Glu	Gln	Gln	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Asn	
		35					40					45				
Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	Pro	
	50					55					60					
Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	Ser	Ile	
65					70					75					80	
Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	
				85					90					95		
Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	
			100					105					110			
Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Tyr	Val	Glu	Gly	Gly	
	115						120					125				
Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	Ser	Thr	Ile	Asn	Pro	
	130					135					140					
Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	Asn	Met	Ala	Thr	Gln	
145					150					155					160	
Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	
				165					170					175		
Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	
			180					185					190			
Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gln	
		195					200					205				
Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	
	210					215					220					
Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	
225				230						235					240	
Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	
			245						250					255		
Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	
			260					265					270			
Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	



275		280		285
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln				
290		295		300
Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu				
305		310		320
Leu Gly Met Ala Pro Ala Leu Gln Pro				
	325			

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Gly Gly Ser Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile			
1	5	10	15
Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn			
	20	25	30
Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu			
	35	40	45
Pro Asn Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala			
	50	55	60
Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser			
65	70	75	80
Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Tyr Val Glu			
	85	90	95
Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile			
	100	105	110
Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala			
	115	120	125
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala			
	130	135	140
Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser			
145	150	155	160
Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly			





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro
		115					120					125			
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser
		130				135					140				
Pro	Asn	Met	Ala	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu
145					150					155					160
Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu
				165					170					175	
Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe
			180					185					190		
Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His
		195					200					205			
Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala
	210					215					220				
Gln	Pro	Gly	Gly	Gly	Ser	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser
225					230					235					240
Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys
				245					250					255	
Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr
			260					265					270		

Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly  
 275 280 285  
 Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu  
 290 295 300  
 Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly  
 305 310 315 320  
 Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 325

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125  
 Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
 130 135 140  
 Pro Asn Met Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val  
 145 150 155 160

Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	165	170	175	
His	Leu	Ala	Gln	Pro	Gly	Gly	Gly	Ser	Asp	Met	Ala	Thr	Pro	Leu	Gly	180	185	190	
Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	195	200	205	
Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	210	215	220	
Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	225	230	235	240
Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	245	250	255	
Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	260	265	270	
Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	275	280	285	
Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	290	295	300	
Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	305	310	315	320
Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala								325			

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	

Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	115	120	125	
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140	
Pro	Asn	Met	Ala	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	145	150	155	160
Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	165	170	175	
Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	180	185	190	
His	Leu	Ala	Gln	Pro	Gly	Gly	Gly	Ser	Asp	Met	Ala	Thr	Pro	Leu	Gly	195	200	205	
Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	210	215	220	
Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	225	230	235	240
Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	245	250	255	
Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	260	265	270	
Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	275	280	285	
Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	290	295	300	
Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	305	310	315	320
Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly								325			

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	115	120	125	
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140	
Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	145	150	155	160
Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	165	170	175	
Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Gly	Gly	180	185	190	
Gly	Ser	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	195	200	205	
Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	210	215	220	
Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	225	230	235	240



Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala  
 245 250 255  
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu  
 260 265 270  
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala  
 275 280 285  
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
 290 295 300  
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
 305 310 315 320  
 Leu Gly Met Ala Pro Ala Leu Gln Pro  
 325

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 319 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys  
 1 5 10 15  
 Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp  
 20 25 30  
 Gln Asp Ile Leu Met Asp Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
 35 40 45  
 Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser  
 50 55 60  
 Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro  
 65 70 75 80  
 Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg  
 85 90 95  
 Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125

Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140	
Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	145	150	155	160
Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	165	170	175	
Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly	180	185	190	
Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	195	200	205	
Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	210	215	220	
Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	225	230	235	240
Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	245	250	255	
Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	260	265	270	
Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	275	280	285	
Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	290	295	300	
Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	305	310	315		

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	1	5	10	15
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	20	25	30	

Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	
		35						40					45			
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	
		50			55					60						
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	
65					70					75					80	
Thr	Arg	His	Pro	Ile	Ile	Ile	Arg	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	
		85						90					95			
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	
		100						105					110			
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	
		115						120					125			
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	
130					135						140					
Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	
145					150					155					160	
Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	
		165						170					175			
Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Thr	Pro	
		180						185					190			
Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	
		195						200					205			
Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	
210					215					220						
Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	
225					230					235					240	
Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	
		245						250					255			
Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	
		260						265					270			
Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	
		275						280					285			
Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	
290					295						300					
Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	
305					310					315					320	
Gln	Pro															

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
			20					25					30		
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
		35					40					45			
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	Ile	Ile	Arg	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro
		115					120					125			
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser
	130					135					140				
Pro	Asn	Met	Ala	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe
145					150					155					160
Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe
				165					170					175	
Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Ser	Gly
			180					185					190		
Gly	Ser	Gly	Gly	Ser	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val
		195					200					205			
Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala
	210					215					220				

Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser
225					230					235					240
Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu
				245					250					255	
Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr
			260					265					270		
Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro
		275					280					285			
Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile
	290					295					300				
Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	
305					310					315					

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
			20					25					30		
Gln	Asp	Ile	Leu	Met	Asp	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
		35					40					45			
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser
		50					55					60			
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro

115	120	125
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser		
130	135	140
Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe		
145	150	155 160
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe		
	165	170 175
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro		
	180	185 190
Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu		
	195	200 205
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys		
	210	215 220
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu		
	225	230 235 240
Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser		
	245	250 255
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu		
	260	265 270
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu		
	275	280 285
Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala		
	290	295 300
Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu		
305	310	315 320
Gln Pro		

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	1	5	10	15
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	20	25	30	
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	35	40	45	
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	50	55	60	
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	65	70	75	80
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	85	90	95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	100	105	110	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	115	120	125	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	130	135	140	
Asn	Met	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	145	150	155	160
Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	165	170	175	
Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	180	185	190	
Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	195	200	205	
Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	210	215	220	
Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	225	230	235	240
Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	245	250	255	
Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	260	265	270	
Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	275	280	285	
Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	290	295	300	

Cys Pro  
305

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 306 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55				60						
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
		130				135					140					
Asn	Met	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	
145					150					155					160	
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	
			165						170					175		
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	
			180					185					190			
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	
		195					200					205				



Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu  
210 215 220

Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe  
225 230 235 240

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
245 250 255

Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Met Ala  
260 265 270

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
275 280 285

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
290 295 300

His Pro  
305

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
1 5 10 15

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
20 25 30

Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
35 40 45

Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
50 55 60

Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
65 70 75 80

Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
85 90 95

Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln

	100		105		110										
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
	115						120					125			
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro
	130						135					140			
Asn	Met	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys
145					150					155					160
Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr
					165				170					175	
Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr
			180					185					190		
Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu
	195						200					205			
Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly
	210					215					220				
Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln
225					230					235					240
His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser
				245					250					255	
Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro
			260					265					270		
Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His
	275						280					285			
Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro
	290					295					300				
Thr	Pro														
305															

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg

1		5		10		15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro
		20				25	
Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
		30					
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu
		35				40	
Pro	Asn	Leu	Glu	Ser	Gly	Ile	Glu
		45					
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu
		50				55	
Ala	Ser	Gly	Ile	Glu	Ala	Ile	
		60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu
		65				70	
Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
		75				80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala
						85	
Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
		90				95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr
		100					
Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
		105				110	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser
		115					
Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
		120				125	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro
		130				135	
Lys	Glu	Ser	His	Lys	Ser	Pro	
		140					
Asn	Met	Ala	Val	Asp	Phe	Ser	Leu
		145				150	
Glu	Trp	Lys	Thr	Gln	Met	Glu	
		155				160	
Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu
		165					
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu
		170				175	
Gly	Val	Met	Ala	Ala	Arg	Gly	Gln
		180					
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser
		185				190	
Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln
		195					
Val	Arg	Leu	Leu	Gly	Ala	Leu	
		200				205	
Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu
		210					
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala
		215				220	
His	Lys	Asp	Pro	Asn	Ala	Ile	Phe
		225				230	
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg
		235				240	
Gly	Lys	Val	Arg	Phe	Leu	Met	Leu
		245					
Gly	Gly	Ser	Thr	Leu	Cys	Val	
		250				255	
Arg	Glu	Phe	Gly	Gly	Asn	Met	Ala
		260					
Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp
		265				270	
Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu
		275					
Arg	Asp	Ser	His	Val	Leu	His	Ser
		280				285	
Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val
		290					
His	Pro	Leu	Pro	Thr	Pro	Val	Leu
		295				300	
Leu	Pro						

305

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 306 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35					40					45			
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50					55				60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70				75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
			85					90						95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
			100					105					110		
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
	115						120					125			
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro
	130					135					140				
Asn	Met	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr
145					150				155					160	
Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val
			165					170						175	
Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu
			180				185						190		
Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser
	195					200						205			
Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys

210		215		220											
Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys
225					230					235					240
Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu
			245						250					255	
Phe	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg
			260					265					270		
Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu
	275						280					285			
Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro
290						295					300				
Ala	Val														
305															

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35					40					45			
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50					55					60				
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70					75				80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
			85						90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
			100					105					110		
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile



20					25					30					
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35					40					45			
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
		50					55					60			
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
		65					70					75			80
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
				85					90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
			100					105					110		
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
		115					120					125			
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro
		130					135					140			
Asn	Met	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly
		145					150					155			160
Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln
			165					170					175		
Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile
			180					185					190		
Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met
		195					200					205			
Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn	Met
		210					215					220			
Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu
		225					230					235			240
Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu
			245					250					255		
Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser
			260					265					270		
Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile
		275					280					285			
Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly
		290					295					300			
Gln	Leu														
		305													

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 306 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70				75					80		
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
	115						120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
	130					135					140					
Asn	Met	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	
145					150				155						160	
Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	
			165						170					175		
Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	
			180					185					190			
Phe	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	
	195						200					205				
Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	
	210					215					220					
Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	





130		135		140
Asn Met Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu				
145		150		155 160
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val				
	165		170	175
Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Met Ala Ser				
	180		185	190
Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg				
	195		200	205
Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His				
	210		215	220
Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly				
	225		230	235 240
Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly				
	245		250	255
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu				
	260		265	270
Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val				
	275		280	285
Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro				
	290		295	300
Pro Gln				
305				

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
1 5 10 15
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val
20 25 30
Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe

35	40	45
Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile		
50	55	60
Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser		
65	70	75
Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu		
	85	90
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln		
	100	105
Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile		
	115	120
Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro		
	130	135
Asn Met Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His		
	145	150
Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr		
	165	170
Leu Cys Val Arg Glu Phe Gly Gly Asn Met Ala Ser Pro Ala Pro Pro		
	180	185
Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val		
	195	200
Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr		
	210	215
Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr		
	225	230
Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu		
	245	250
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys		
	260	265
Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu		
	275	280
Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg		
	290	295
Thr Thr		
305		

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
	115						120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
	130					135					140					
Asn	Met	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	
145					150					155					160	
Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	
				165					170					175		
Arg	Glu	Phe	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	
			180					185					190			
Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	
		195					200					205				
Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	
	210					215					220					
Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	
225					230					235					240	
Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	

	245		250		255
Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser					
	260		265		270
Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu					
	275		280		285
Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala					
	290		295		300
His Lys					
305					

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg					
1	5	10	15		
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val					
	20	25	30		
Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe					
	35	40	45		
Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile					
	50	55	60		
Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser					
	65	70	75		80
Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu					
	85	90	95		
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln					
	100	105	110		
Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile					
	115	120	125		
Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro					
	130	135	140		
Asn Met Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val					

145		150		155		160									
Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe
				165					170					175	
Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val
			180					185					190		
Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser
		195					200					205			
Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala
	210					215					220				
Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys
225					230					235					240
Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met
			245					250						255	
Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly
			260					265					270		
Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu
		275					280					285			
Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp
	290					295					300				
Pro	Asn														
305															

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35				40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile

50

55

60

Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80  
 Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
 85 90 95  
 Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110  
 Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125  
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val  
 145 150 155 160  
 Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala  
 165 170 175  
 Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala  
 180 185 190  
 Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln  
 195 200 205  
 Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu  
 210 215 220  
 Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro  
 225 230 235 240  
 Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg  
 245 250 255  
 Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly  
 260 265 270  
 Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser  
 275 280 285  
 Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys  
 290 295 300  
 Pro  
 305

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
	130					135						140				
Asn	Met	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	
145					150					155					160	
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	
			165						170					175		
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	
			180					185					190			
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	
		195					200					205				
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	
	210					215						220				
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	
225					230					235					240	
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	
				245					250					255		



Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Asn	Met	Ala	Ser
			260					265					270		
Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg
		275					280					285			
Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His
	290					295					300				
Pro															
305															

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35					40					45			
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50					55					60				
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70				75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
			85						90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
			100					105					110		
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
		115					120					125			
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro
	130					135					140				
Asn	Met	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys
145					150					155					160

Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr  
 165 170 175  
 Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr  
 180 185 190  
 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu  
 195 200 205  
 Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly  
 210 215 220  
 Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln  
 225 230 235 240  
 His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser  
 245 250 255  
 Thr Leu Cys Val Arg Glu Phe Gly Asn Met Ala Ser Pro Ala Pro Pro  
 260 265 270  
 Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val  
 275 280 285  
 Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr  
 290 295 300  
 Pro  
 305

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30  
 Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60

Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
	130					135					140					
Asn	Met	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	
145					150					155					160	
Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	
				165					170						175	
Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	
			180					185					190			
Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	
		195					200						205			
Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	
	210					215					220					
His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	
225					230					235					240	
Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	
				245					250					255		
Arg	Glu	Phe	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	
			260					265					270			
Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	
		275					280					285				
Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	
	290					295					300					
Pro																
305																

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
	115						120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
	130					135					140					
Asn	Met	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	
145					150					155					160	
Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	
			165					170						175		
Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	
			180					185					190			
Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	
	195					200						205				
Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	
	210					215					220					
Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	
225				230						235					240	
Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	
			245						250					255		
Phe	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	
			260					265					270			

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser  
 275 280 285

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala  
 290 295 300

Val  
 305

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30

Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45

Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60

Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80

Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
 85 90 95

Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140

Asn Met Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp  
 145 150 155 160

Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg  
 165 170 175

Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	180	185	190	
Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	195	200	205	
Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	210	215	220	
Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	225	230	235	240
Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Asn	Met	245	250	255	
Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	260	265	270	
Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	275	280	285	
Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	290	295	300	
Leu																305			

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	1	5	10	15
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	20	25	30	
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	35	40	45	
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	50	55	60	
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	65	70	75	80

Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu		
			85						90					95			
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln		
			100					105					110				
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile		
		115					120					125					
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro		
	130					135					140						
Asn	Met	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly		
145					150					155					160		
Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln		
			165						170					175			
Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile		
			180					185					190				
Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met		
		195					200					205					
Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Asn	Met	Ala		
	210					215					220						
Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu		
225					230					235				240			
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val		
			245						250					255			
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu		
		260					265						270				
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu		
	275						280					285					
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln		
	290					295					300						
Leu																	
305																	

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
		50				55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
		130				135					140					
Asn	Met	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	
145					150					155					160	
Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	
				165					170					175		
Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	
			180					185					190			
Phe	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	
		195					200					205				
Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	
		210				215					220					
Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	
225					230					235					240	
Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	
				245					250					255		
Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	
			260					265					270			
Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	



275		280		285
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu				
290		295		300
Leu				
305				

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg			
1	5	10	15
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val			
20	25	30	
Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe			
35	40	45	
Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile			
50	55	60	
Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser			
65	70	75	80
Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu			
85	90	95	
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln			
100	105	110	
Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile			
115	120	125	
Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro			
130	135	140	
Asn Met Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu			
145	150	155	160
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val			
165	170	175	
Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Asn Met Ala Ser Pro			

	180		185		190										
Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp
	195						200					205			
Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro
	210					215					220				
Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu
225					230					235					240
Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala
				245					250					255	
Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly
			260					265					270		
Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg
		275					280					285			
Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro
	290					295					300				
Gln															
305															

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5				10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35					40				45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50					55					60				
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70				75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu

85										90					95															
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln															
			100						105					110																
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile															
		115					120					125																		
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro															
	130					135					140																			
Asn	Met	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu															
145					150					155					160															
Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val															
				165					170					175																
Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Asn	Met	Ala	Ser	Pro															
			180					185					190																	
Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp															
		195					200					205																		
Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro															
	210					215					220																			
Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu															
225					230					235				240																
Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala															
				245					250					255																
Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly															
			260					265					270																	
Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg															
		275					280					285																		
Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro															
	290					295					300																			
Gln																														
305																														

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
	130					135						140				
Asn	Met	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	
145					150					155					160	
Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	
				165					170					175		
Arg	Glu	Phe	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	
			180					185					190			
Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	
		195					200					205				
Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	
	210					215					220					
Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	
225					230					235				240		
Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	
				245					250					255		
Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	
			260					265					270			
Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
		275					280					285				
Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	

290

295

300

Lys  
305

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg			
1				5					10					15				
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val			
			20					25					30					
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe			
		35				40					45							
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile			
	50				55					60								
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser			
65				70					75					80				
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu			
			85						90					95				
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln			
			100					105					110					
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile			
		115					120					125						
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro			
	130					135					140							
Asn	Met	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val			
145				150						155				160				
Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe			
			165					170						175				
Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu			
																180	185	190

Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln
		195					200					205			
Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val
		210				215					220				
Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala
225					230					235					240
Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala
				245				250						255	
Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln
			260					265					270		
Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu
		275				280						285			
Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro
	290					295					300				
Asn															
305															

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35				40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50					55				60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70					75					80
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
			85						90						95

Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110  
 Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125  
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
 145 150 155 160  
 Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
 165 170 175  
 Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
 180 185 190  
 Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln  
 195 200 205  
 Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu  
 210 215 220  
 Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe  
 225 230 235 240  
 Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
 245 250 255  
 Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Gly Gly  
 260 265 270  
 Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser  
 275 280 285  
 Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys  
 290 295 300  
 Pro Glu Val His Pro  
 305

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	1	5	10	15
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	20	25	30	
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	35	40	45	
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	50	55	60	
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	65	70	75	80
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	85	90	95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	100	105	110	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	115	120	125	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	130	135	140	
Asn	Met	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	145	150	155	160
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	165	170	175	
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	180	185	190	
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	195	200	205	
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	210	215	220	
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	225	230	235	240
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	245	250	255	
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn	Gly	Gly	260	265	270	
Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	275	280	285	
Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	290	295	300	



Pro Glu Val His Pro  
305

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 309 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
		130				135						140				
Asn	Met	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	
145					150					155					160	
Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	
			165						170					175		
Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	
			180					185					190			
Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	
		195					200					205				

Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly
210						215					220				
Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln
225					230					235					240
His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser
				245					250					255	
Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn	Gly	Gly	Asn	Met	Ala	Ser
			260					265					270		
Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg
		275					280					285			
Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His
	290					295					300				
Pro	Leu	Pro	Thr	Pro											
305															

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35				40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50				55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65				70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
			85						90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
			100					105					110		

Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	115	120	125	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	130	135	140	
Asn	Met	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	145	150	155	160
Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	165	170	175	
Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	180	185	190	
Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	195	200	205	
Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	210	215	220	
His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	225	230	235	240
Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	245	250	255	
Arg	Glu	Phe	Gly	Gly	Asn	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	260	265	270	
Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	275	280	285	
Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	290	295	300	
Pro	Val	Leu	Leu	Pro												305			

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	20	25	30	
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	35	40	45	
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	50	55	60	
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	65	70	75	80
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	85	90	95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	100	105	110	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	115	120	125	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	130	135	140	
Asn	Met	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	145	150	155	160
Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	165	170	175	
Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	180	185	190	
Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	195	200	205	
Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	210	215	220	
Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	225	230	235	240
Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	245	250	255	
Phe	Gly	Gly	Asn	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	260	265	270	
Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	275	280	285	
Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	290	295	300	
Leu	Leu	Pro	Ala	Val												305			

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 309 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25					30			
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
	50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70					75					80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
	130					135					140					
Asn	Met	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	
145					150					155					160	
Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	
			165						170					175		
Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	
			180					185					190			
Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	
		195					200					205				
Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	
	210					215					220					

Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu
225					230					235					240
Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn
			245						250					255	
Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val
			260					265					270		
Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser
		275					280					285			
Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala
	290					295					300				
Val	Asp	Phe	Ser	Leu											
305															

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35					40					45			
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50					55					60				
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70					75				80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
			85						90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
			100					105					110		
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
		115					120					125			

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly  
 145 150 155 160  
 Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln  
 165 170 175  
 Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile  
 180 185 190  
 Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met  
 195 200 205  
 Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Gly  
 210 215 220  
 Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu  
 225 230 235 240  
 Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln  
 245 250 255  
 Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val  
 260 265 270  
 Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala  
 275 280 285  
 Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala  
 290 295 300  
 Ala Arg Gly Gln Leu  
 305

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30





(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 309 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	
1				5					10					15		
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	
			20					25						30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	
		35					40					45				
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	
		50				55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	
65					70				75						80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	
			85						90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
			100					105					110			
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	
		115					120					125				
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	
		130				135					140					
Asn	Met	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	
145					150				155						160	
Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	
				165					170				175			
Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	Gly	Gly	Asn	Gly	Gly	Asn	
			180					185					190			
Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	
		195					200					205				
Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	
		210				215					220					
Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	

225		230		235		240									
Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp
				245					250					255	
Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg
			260					265						270	
Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser
		275					280					285			
Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr
	290					295					300				
Gln	Leu	Pro	Pro	Gln											
305															

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg
1				5					10					15	
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val
			20					25					30		
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe
		35					40					45			
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
	50					55					60				
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70					75				80	
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
			85					90						95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
		100						105					110		
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
		115					120					125			
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro



35					40					45					
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile
50					55					60					
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser
65					70					75					80
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu
				85					90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln
			100					105					110		
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
		115					120					125			
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro
		130					135					140			
Asn	Met	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg
145					150					155					160
Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val
				165					170					175	
Arg	Glu	Phe	Gly	Gly	Asn	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro
			180					185					190		
Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val
		195					200					205			
Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr
	210					215					220				
Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr
225					230					235					240
Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu
				245					250					255	
Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys
			260					265					270		
Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu
		275					280					285			
Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg
		290					295					300			
Thr	Thr	Ala	His	Lys											
305															

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	1	5	10	15
Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	Val	20	25	30	
Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	35	40	45	
Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	50	55	60	
Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	65	70	75	80
Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	85	90	95	
Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	100	105	110	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	115	120	125	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	130	135	140	
Asn	Met	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	145	150	155	160
Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Glu	Phe	165	170	175	
Gly	Gly	Asn	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	180	185	190	
Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	195	200	205	
Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	210	215	220	
Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	225	230	235	240



Asn	Met	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg
145					150					155					160
Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val
				165					170					175	
Arg	Glu	Phe	Gly	Gly	Asn	Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp
			180					185						190	
Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser
		195					200					205			
Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu
	210					215					220				
Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu
225					230					235					240
Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu
				245					250						255
Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser
			260					265					270		
Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu
		275					280						285		
Gln	Ser	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys		
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

AATTCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT 60

ACGTAGAGGG CGGTGGAGGC TCC 83

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

CCGGGGAGCC TCCACGCCC TCTACGTACT GTTGAAGCCTG CGCGTTCTCC AAGGTTTCA 60

GATAGAAGGT CAGTTTACGA CGG 83

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Gly Gly Gly Ser Gly Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Ser Gly Gly Ser Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Glu Phe Gly Asn Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Glu Phe Gly Gly Asn Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Glu Phe Gly Gly Asn Gly Gly Asn Met Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Gly Gly Ser Asp Met Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 459 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown  
  
(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT	60
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCTG	120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA	180
CAGGACATTC TGGGAGCAGT GACCCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA	240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC	300
CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT	360
CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT	420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCCTCAGG	459

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA	60
CTCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTG	120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCA	180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGG	240
GGACCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTC	300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGGGCAGGA CCACAGCTCA CAAG	360
GATCCC AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT	420
CCTGATGCTT GTAGGAGGGT CCACCTCTG CGTCAGG	447

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TCCCCAGCGC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA	60
CTCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTG	120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCA	180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGG	240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC 300  
 CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT 360  
 CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT 420  
 TTCCTGATGC TTGTAGGAGG GTCCACCCTC TCGTCAGG 459

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 153 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	1	5	10	15
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	20	25	30	
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	35	40	45	
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	50	55	60	
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	65	70	75	80
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	85	90	95	
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	100	105	110	
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	115	120	125	
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	130	135	140	
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	145	150									

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu
1				5					10					15	
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val
			20					25					30		
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu
		35					40					45			
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu
	50					55					60				
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln
65					70				75						80
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln
				85					90					95	
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Gly
			100					105					110		
Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln
			115				120					125			
His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser
	130					135					140				
Thr	Leu	Cys	Val	Arg											
145															

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu

1	5	10	15
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val	20	25	30
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu	35	40	45
Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu	50	55	60
Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln	65	70	75
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln	85	90	95
Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu	100	105	110
Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe	115	120	125
Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu	130	135	140
Val Gly Gly Ser Thr Leu Cys Val Arg	145	150	

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GGATCCACCA TGAGCCGCCT GCCCGTCCTG CTCCTGCTCC AACTCCTGGT CCGCCCCGCC	60
ATGG	64

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 112  
 (D) OTHER INFORMATION: /note= "position 112 is deleted or Leu, Ala,Val, Ile, Pro, Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 113  
 (D) OTHER INFORMATION: /note= "positoin 113 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 114  
 (D) OTHER INFORMATION: /note= "position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 115  
 (D) OTHER INFORMATION: /note= "positon 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or Asn"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	1	5	10	15
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	20	25	30	
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	35	40	45	
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	50	55	60	
Gly	Ala	Val	Thr	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	65	70	75	80	
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	85	90	95	
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Xaa	100	105	110	
Xaa	Xaa	Xaa	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	115	120	125	
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	130	135	140	

Val Gly Gly Ser Thr Leu Cys Val Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

CCATGGCTAA CTGCTCTATA ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG	60
CACCTTTGCT GGACCCGAAC AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGATCGAA	120
ACCTTCGACT TCCAAACCTG GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT	180
CAGGTATTGA GGCAATTCTT CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC	240
CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAACTGA	300
CGTTCTATCT GGTTACCCCTT GAGCAAGCGC AGGAACAACA GTACGTAGAG GGCGGTGGAG	360
GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT CCGTCTAAAG	420
AATCTCATAA ATCTCCAAAC ATGTAAGGTA CCGCATGCAA GCTT	464

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

AAAACAAGAA GAAAGGCGAT AAAAAGGTTG TGGTAAGAGA AATGGATAAA AAGGGGTCGG	60
GGAAGGAAGG TGGGAGTTAA AAAAGAGGAA GTAGGTCAAG	100

(2) INFORMATION FOR SEQ ID NO:259:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11808 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

ACGTACTCCA TGGCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA	60
CCACCTGCAC CTTTGCTGGA CCCGAACAAC CTCAATGACG AAGACGTCTC TATCCTGATG	120
GATCGAAACC TTCGACTTCC AAACCTGGAG AGCTTCGTAA GGGCTGTCAA GAACTTAGAA	180
AATGCATCAG GTATTGAGGC AATTCTTCGT AATCTCCAAC CATGTCTGCC CTCTGCCACG	240
GCCGCACCTT CTCGACATCC AATCATCATC AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA	300
AAACTGACGT TCTATCTGGT TACCCTTGAG CAAGCGCAGG AACAAACAGTA CGTAGAGGGC	360
GGTGGAGGCT CCCCAGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG	420
TCTAAAGAAT CTCATAAATC TCCAAACATG GCTTTAGGCC CTGCCAGCTC CCTGCCCCAG	480
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC	540
CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA	600
CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG	660
GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC	720
CTGGAAGGGA TATCCCCCGA GTTGGGTCCC ACCTTGACA CACTGCAGCT GGACGTCGCC	780
GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG	840
CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC	900
CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCGT ACCGCGTTCT ACGCCACCTT	960
GCGCAGCCCG ACATGGCTAC ACCAACGTAC TCCATGGCTA ACTGCTCTAT AATGATCGAT	1020
GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT	1080
GACGAAGACG TCTCTATCCT GATGGATCGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC	1140
GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	1200
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	1260
GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG	1320

CAGGAACAAC	AGTACGTAGA	GGGCGGTGGA	GGCTCCCCGG	GTGAACCGTC	TGGTCCAATC	1380
TCTACTATCA	ACCCGTCTCC	TCCGTCTAAA	GAATCTCATA	AATCTCCAAA	CATGGCTCAG	1440
AGCTTCCTGC	TCAAGTCTTT	AGAGCAAGTG	AGGAAGATCC	AGGGCGATGG	CGCAGCGCTC	1500
CAGGAGAAGC	TGTGTGCCAC	CTACAAGCTG	TGCCACCCCG	AGGAGCTGGT	GCTGCTCGGA	1560
CACTCTCTGG	GCATCCCCTG	GGCTCCCCTG	AGCTCCTGCC	CCAGCCAGGC	CCTGCAGCTG	1620
GCAGGCTGCT	TGAGCCAACT	CCATAGCGGC	CTTTTCCTCT	ACCAGGGGCT	CCTGCAGGCC	1680
CTGGAAGGGA	TATCCCCCGA	GTTGGGTCCC	ACCTTGGACA	CACTGCAGCT	GGACGTCGCC	1740
GACTTTGCCA	CCACCATCTG	GCAGCAGATG	GAAGAACTGG	GAATGGCCCC	TGCCCTGCAG	1800
CCCACCCAGG	GTGCCATGCC	GGCCTTCGCC	TCTGCTTTCC	AGCGCCGGGC	AGGAGGGGTC	1860
CTGGTTGCTA	GCCATCTGCA	GAGCTTCCTG	GAGGTGTCGT	ACCGCGTTCT	ACGCCACCTT	1920
GCGCAGCCCC	ACATGGCTAC	ACCATTAGGC	CCTGCCAGCT	CCCTGCCCCAC	GTACTIONCATG	1980
GCTAACTGCT	CTATAATGAT	CGATGAAATT	ATACATCACT	TAAAGAGACC	ACCTGCACCT	2040
TTGCTGGACC	CGAACAACCT	CAATGACGAA	GACGTCTCTA	TCCTGATGGA	TCGAAACCTT	2100
CGACTTCCAA	ACCTGGAGAG	CTTCGTAAGG	GCTGTCAAGA	ACTTAGAAAA	TGCATCAGGT	2160
ATTGAGGCAA	TTCTTCGTAA	TCTCCAACCA	TGTCTGCCCT	CTGCCACGGC	CGCACCCCTCT	2220
CGACATCCAA	TCATCATCAA	GGCAGGTGAC	TGGCAAGAAT	TCCGGGAAAA	ACTGACGTTC	2280
TATCTGGTTA	CCCTTGAGCA	AGCGCAGGAA	CAACAGTACG	TAGAGGGCGG	TGGAGGCTCC	2340
CCGGGTGAAC	CGTCTGGTCC	AATCTCTACT	ATCAACCCGT	CTCCTCCGTC	TAAAGAATCT	2400
CATAAATCTC	CAAACATGGC	TTTCCTGCTC	AAGTCTTTAG	AGCAAGTGAG	GAAGATCCAG	2460
GGCGATGGCG	CAGCGCTCCA	GGAGAAGCTG	TGTGCCACCT	ACAAGCTGTG	CCACCCCGAG	2520
GAGCTGGTGC	TGCTCGGACA	CTCTCTGGGC	ATCCCCTGGG	CTCCCCTGAG	CTCCTGCCCC	2580
AGCCAGGCCC	TGCAGCTGGC	AGGCTGCTTG	AGCCAACTCC	ATAGCGGCCT	TTTCCTCTAC	2640
CAGGGGCTCC	TGCAGGCCCT	GGAAGGGATA	TCCCCCGAGT	TGGGTCCCAC	CTTGGACACA	2700
CTGCAGCTGG	ACGTCGCCGA	CTTTGCCACC	ACCATCTGGC	AGCAGATGGA	AGAACTGGGA	2760
ATGGCCCCCTG	CCCTGCAGCC	CACCCAGGGT	GCCATGCCGG	CCTTCGCCTC	TGCTTTCCAG	2820
CGCCGGGCAG	GAGGGGTCTC	GGTTGCTAGC	CATCTGCAGA	GCTTCCTGGA	GGTGTGCTAC	2880
CGCGTTCTAC	GCCACCTTGC	GCAGCCCCGAC	ATGGCTACAC	CATTAGGCCC	TGCCAGCTCC	2940
CTGCCCCAGA	GCACGTACTC	CATGGCTAAC	TGCTCTATAA	TGATCGATGA	AATTATACAT	3000

CACTTAAAGA	GACCACCTGC	ACCTTTGCTG	GACCCGAACA	ACCTCAATGA	CGAAGACGTC	3060
TCTATCCTGA	TGGATCGAAA	CCTTCGACTT	CCAAACCTGG	AGAGCTTCGT	AAGGGCTGTC	3120
AAGAACTTAG	AAAATGCATC	AGGTATTGAG	GCAATTCTTC	GTAATCTCCA	ACCATGTCTG	3180
CCCTCTGCCA	CGGCCGCACC	CTCTCGACAT	CCAATCATCA	TCAAGGCAGG	TGACTGGCAA	3240
GAATTCCGGG	AAAAACTGAC	GTTCTATCTG	GTTACCCTTG	AGCAAGCGCA	GGAACAACAG	3300
TACGTAGAGG	GCGGTGGAGG	CTCCCCGGGT	GAACCGTCTG	GTCCAATCTC	TACTATCAAC	3360
CCGTCTCCTC	CGTCTAAAGA	ATCTCATAAA	TCTCCAAACA	TGGCTGAGCA	AGTGAGGAAG	3420
ATCCAGGGCG	ATGGCGCAGC	GCTCCAGGAG	AAGCTGTGTG	CCACCTACAA	GCTGTGCCAC	3480
CCCGAGGAGC	TGGTGCTGCT	CGGACACTCT	CTGGGCATCC	CCTGGGCTCC	CCTGAGCTCC	3540
TGCCCCAGCC	AGGCCCTGCA	GCTGGCAGGC	TGCTTGAGCC	AACTCCATAG	CGGCCTTTTC	3600
CTCTACCAGG	GGCTCCTGCA	GGCCCTGGAA	GGGATATCCC	CCGAGTTGGG	TCCCACCTTG	3660
GACACACTGC	AGCTGGACGT	CGCCGACTTT	GCCACCACCA	TCTGGCAGCA	GATGGAAGAA	3720
CTGGGAATGG	CCCCTGCCCT	GCAGCCCACC	CAGGGTGCCA	TGCCGGCCTT	CGCCTCTGCT	3780
TTCCAGCGCC	GGGCAGGAGG	GGTCCTGGTT	GCTAGCCATC	TGCAGAGCTT	CCTGGAGGTG	3840
TCGTACCGCG	TTCTACGCCA	CCTTGCGCAG	CCCGACATGG	CTACACCATT	AGGCCCTGCC	3900
AGCTCCCTGC	CCCAGAGCTT	CCTGCTCAAG	TCTTTAACGT	ACTCCATGGC	TAAGTGTCTT	3960
ATAATGATCG	ATGAAATTAT	ACATCACTTA	AAGAGACCAC	CTGCACCTTT	GCTGGACCCG	4020
AACAACCTCA	ATGACGAAGA	CGTCTCTATC	CTGATGGATC	GAAACCTTCG	ACTTCCAAAC	4080
CTGGAGAGCT	TCGTAAGGGC	TGTCAAGAAC	TTAGAAAATG	CATCAGGTAT	TGAGGCAATT	4140
CTTCGTAATC	TCCAACCATG	TCTGCCCTCT	GCCACGGCCG	CACCCTCTCG	ACATCCAATC	4200
ATCATCAAGG	CAGGTGACTG	GCAAGAATTC	CGGGAAAAAC	TGACGTTCTA	TCTGGTTACC	4260
CTTGAGCAAG	CGCAGGAACA	ACAGTACGTA	GAGGGCGGTG	GAGGCTCCCC	GGGTGAACCG	4320
TCTGGTCCAA	TCTCTACTAT	CAACCCGTCT	CCTCCGTCTA	AAGAATCTCA	TAAATCTCCA	4380
AACATGGCTC	TGCTCGGACA	CTCTCTGGGC	ATCCCCTGGG	CTCCCCTGAG	CTCCTGCCCC	4440
AGCCAGGCCC	TGCAGCTGGC	AGGCTGCTTG	AGCCAACTCC	ATAGCGGCCT	TTTCCTCTAC	4500
CAGGGGCTCC	TGCAGGCCCT	GGAAGGGATA	TCCCCCGAGT	TGGGTCCCAC	CTTGACACA	4560
CTGCAGCTGG	ACGTCGCCGA	CTTTGCCACC	ACCATCTGGC	AGCAGATGGA	AGAACTGGGA	4620
ATGGCCCCCTG	CCCTGCAGCC	CACCCAGGGT	GCCATGCCGG	CCTTCGCCTC	TGCTTTCCAG	4680
CGCCGGGCAG	GAGGGGTCCT	GGTTGCTAGC	CATCTGCAGA	GCTTCCTGGA	GGTGTCGTAC	4740

CGCGTTCTAC	GCCACCTTGC	GCAGCCCGAC	ATGGCTACAC	CATTAGGCCC	TGCCAGCTCC	4800
CTGCCCCAGA	GCTTCCTGCT	CAAGTCTTTA	GAGCAAGTGA	GGAAGATCCA	GGGCGATGGC	4860
GCAGCGCTCC	AGGAGAAGCT	GTGTGCCACC	TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	4920
ACGTACTCCA	TGGCTAACTG	CTCTATAATG	ATCGATGAAA	TTATACATCA	CTTAAAGAGA	4980
CCACCTGCAC	CTTTGCTGGA	CCCGAACAAC	CTCAATGACG	AAGACGTCTC	TATCCTGATG	5040
GATCGAAACC	TTCGACTTCC	AAACCTGGAG	AGCTTCGTAA	GGGCTGTCAA	GAACCTAGAA	5100
AATGCATCAG	GTATTGAGGC	AATTCTTCGT	AATCTCCAAC	CATGTCTGCC	CTCTGCCACG	5160
GCCGCACCTT	CTCGACATCC	AATCATCATC	AAGGCAGGTG	ACTGGCAAGA	ATTCCGGGAA	5220
AAACTGACGT	TCTATCTGGT	TACCCTTGAG	CAAGCGCAGG	AACAACAGTA	CGTAGAGGGC	5280
GGTGGAGGCT	CCCCGGGTGA	ACCGTCTGGT	CCAATCTCTA	CTATCAACCC	GTCTCCTCCG	5340
TCTAAAGAAT	CTCATAAATC	TCCAAACATG	GCTCCCCTGA	GCTCCTGCCC	CAGCCAGGCC	5400
CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	CATAGCGGCC	TTTTCTCTTA	CCAGGGGCTC	5460
CTGCAGGCCC	TGGAAGGGAT	ATCCCCCGAG	TTGGGTCCCA	CCTTGGACAC	ACTGCAGCTG	5520
GACGTCGCCG	ACTTTGCCAC	CACCATCTGG	CAGCAGATGG	AAGAACTGGG	AATGGCCCCT	5580
GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	GCCTTCGCCT	CTGCTTTCCA	GCGCCGGGCA	5640
GGAGGGGTCC	TGGTTGCTAG	CCATCTGCAG	AGCTTCCTGG	AGGTGTCGTA	CCGCGTTCTA	5700
CGCCACCTTG	CGCAGCCCGA	CATGGCTACA	CCATTAGGCC	CTGCCAGCTC	CCTGCCCCAG	5760
AGCTTCCTGC	TCAAGTCTTT	AGAGCAAGTG	AGGAAGATCC	AGGGCGATGG	CGCAGCGCTC	5820
CAGGAGAAGC	TGTGTGCCAC	CTACAAGCTG	TGCCACCCCG	AGGAGCTGGT	GCTGCTCGGA	5880
CACTCTCTGG	GCATCCCCTG	GGCTACGTAC	TCCATGGCTA	ACTGCTCTAT	AATGATCGAT	5940
GAAATTATAC	ATCACTTAAA	GAGACCACCT	GCACCTTTGC	TGGACCCGAA	CAACCTCAAT	6000
GACGAAGACG	TCTCTATCCT	GATGGATCGA	AACCTTCGAC	TTCCAAACCT	GGAGAGCTTC	6060
GTAAGGGCTG	TCAAGAACTT	AGAAAATGCA	TCAGGTATTG	AGGCAATTCT	TCGTAATCTC	6120
CAACCATGTC	TGCCCTCTGC	CACGGCCGCA	CCCTCTCGAC	ATCCAATCAT	CATCAAGGCA	6180
GGTGACTGGC	AAGAATTCCG	GGAAAACTG	ACGTTCTATC	TGGTTACCCT	TGAGCAAGCG	6240
CAGGAACAAC	AGTACGTAGA	GGGCGGTGGA	GGCTCCCCGG	GTGAACCGTC	TGGTCCAATC	6300
TCTACTATCA	ACCCGTCTCC	TCCGTCTAAA	GAATCTCATA	AATCTCCAAA	CATGGCTCAG	6360
GCCCTGCAGC	TGGCAGGCTG	CTTGAGCCAA	CTCCATAGCG	GCCTTTTCCT	CTACCAGGGG	6420

CTCCTGCAGG	CCCTGGAAGG	GATATCCCCC	GAGTTGGGTC	CCACCTTGGA	CACACTGCAG	6480
CTGGACGTCG	CCGACTTTGC	CACCACCATC	TGGCAGCAGA	TGGAAGAACT	GGGAATGGCC	6540
CCTGCCCTGC	AGCCCACCCA	GGGTGCCATG	CCGGCCTTCG	CCTCTGCTTT	CCAGCGCCGG	6600
GCAGGAGGGG	TCCTGGTTGC	TAGCCATCTG	CAGAGCTTCC	TGGAGGTGTC	GTACCGCGTT	6660
CTACGCCACC	TTGCGCAGCC	CGACATGGCT	ACACCATTAG	GCCCTGCCAG	CTCCCTGCCC	6720
CAGAGCTTCC	TGCTCAAGTC	TTTAGAGCAA	GTGAGGAAGA	TCCAGGGCGA	TGGCGCAGCG	6780
CTCCAGGAGA	AGCTGTGTGC	CACCTACAAG	CTGTGCCACC	CCGAGGAGCT	GGTGCTGCTC	6840
GGACACTCTC	TGGGCATCCC	CTGGGCTCCC	CTGAGCTCCT	GCCCCAGCAC	GTACTCCATG	6900
GCTAACTGCT	CTATAATGAT	CGATGAAATT	ATACATCACT	TAAAGAGACC	ACCTGCACCT	6960
TTGCTGGACC	CGAACAACCT	CAATGACGAA	GACGTCTCTA	TCCTGATGGA	TCGAAACCTT	7020
CGACTTCCAA	ACCTGGAGAG	CTTCGTAAGG	GCTGTCAAGA	ACTTAGAAAA	TGCATCAGGT	7080
ATTGAGGCAA	TTCTTCGTAA	TCTCCAACCA	TGTCTGCCCT	CTGCCACGGC	CGCACCCCTCT	7140
CGACATCCAA	TCATCATCAA	GGCAGGTGAC	TGGCAAGAAT	TCCGGGAAAA	ACTGACGTTC	7200
TATCTGGTTA	CCCTTGAGCA	AGCGCAGGAA	CAACAGTACG	TAGAGGGCGG	TGGAGGCTCC	7260
CCGGGTGAAC	CGTCTGGTCC	AATCTCTACT	ATCAACCCGT	CTCCTCCGTC	TAAAGAATCT	7320
CATAAATCTC	CAAACATGGC	TCTGCAGCTG	GCAGGCTGCT	TGAGCCAACT	CCATAGCGGC	7380
CTTTTCCTCT	ACCAGGGGCT	CCTGCAGGCC	CTGGAAGGGA	TATCCCCCGA	GTTGGGTCCC	7440
ACCTTGACAA	CACTGCAGCT	GGACGTCGCC	GACTTTGCCA	CCACCATCTG	GCAGCAGATG	7500
GAAGAACTGG	GAATGGCCCC	TGCCCTGCAG	CCCACCCAGG	GTGCCATGCC	GGCCTTCGCC	7560
TCTGCTTTCC	AGCGCCGGGC	AGGAGGGGTC	CTGGTTGCTA	GCCATCTGCA	GAGCTTCCTG	7620
GAGGTGTCGT	ACCGCGTTCT	ACGCCACCTT	GCGCAGCCCG	ACATGGCTAC	ACCATTAGGC	7680
CCTGCCAGCT	CCCTGCCCCA	GAGCTTCCTG	CTCAAGTCTT	TAGAGCAAGT	GAGGAAGATC	7740
CAGGGCGATG	GCGCAGCGCT	CCAGGAGAAG	CTGTGTGCCA	CCTACAAGCT	GTGCCACCCC	7800
GAGGAGCTGG	TGCTGCTCGG	ACACTCTCTG	GGCATCCCCT	GGGCTCCCCT	GAGCTCCTGC	7860
CCCAGCCAGG	CCACGTACTC	CATGGCTAAC	TGCTCTATAA	TGATCGATGA	AATTATACAT	7920
CACTTAAAGA	GACCACCTGC	ACCTTTGCTG	GACCCGAACA	ACCTCAATGA	CGAAGACGTC	7980
TCTATCCTGA	TGGATCGAAA	CCTTCGACTT	CCAAACCTGG	AGAGCTTCGT	AAGGGCTGTC	8040
AAGAACTTAG	AAAATGCATC	AGGTATTGAG	GCAATTCTTC	GTAATCTCCA	ACCATGTCTG	8100

CCCTCTGCCA	CGGCCGCACC	CTCTCGACAT	CCAATCATCA	TCAAGGCAGG	TGACTGGCAA	8160
GAATTCCGGG	AAAAACTGAC	GTTCTATCTG	GTTACCCCTG	AGCAAGCGCA	GGAACAACAG	8220
TACGTAGAGG	GCGGTGGAGG	CTCCCCGGGT	GAACCGTCTG	GTCCAATCTC	TACTATCAAC	8280
CCGTCTCCTC	CGTCTAAAGA	ATCTCATAAA	TCTCCAAACA	TGGCTCTGGC	AGGCTGCTTG	8340
AGCCAACTCC	ATAGCGGCCT	TTTCTCTAC	CAGGGGCTCC	TGCAGGCCCT	GGAAGGGATA	8400
TCCCCGAGT	TGGGTCCCAC	CTTGACACA	CTGCAGCTGG	ACGTCGCCGA	CTTTGCCACC	8460
ACCATCTGGC	AGCAGATGGA	AGAACTGGGA	ATGGCCCCTG	CCCTGCAGCC	CACCCAGGGT	8520
GCCATGCCGG	CCTTCGCCTC	TGCTTTCCAG	CGCCGGGCAG	GAGGGGTCCT	GGTTGCTAGC	8580
CATCTGCAGA	GCTTCCTGGA	GGTGTCGTAC	CGCGTTCTAC	GCCACCTTGC	GCAGCCCGAC	8640
ATGGCTACAC	CATTAGGCCC	TGCCAGCTCC	CTGCCCCAGA	GCTTCCTGCT	CAAGTCTTTA	8700
GAGCAAGTGA	GGAAGATCCA	GGGCGATGGC	GCAGCGCTCC	AGGAGAAGCT	GTGTGCCACC	8760
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCCTGG	8820
GCTCCCCTGA	GCTCCTGCCC	CAGCCAGGCC	CTGCAGACGT	ACTCCATGGC	TAACTGCTCT	8880
ATAATGATCG	ATGAAATTAT	ACATCACTTA	AAGAGACCAC	CTGCACCTTT	GCTGGACCCG	8940
AACAACCTCA	ATGACGAAGA	CGTCTCTATC	CTGATGGATC	GAAACCTTCG	ACTTCCAAAC	9000
CTGGAGAGCT	TCGTAAGGGC	TGTCAAGAAC	TTAGAAAATG	CATCAGGTAT	TGAGGCAATT	9060
CTTCGTAATC	TCCAACCATG	TCTGCCCTCT	GCCACGGCCG	CACCCTCTCG	ACATCCAATC	9120
ATCATCAAGG	CAGGTGACTG	GCAAGAATTC	CGGGAAAAAC	TGACGTTCTA	TCTGGTTACC	9180
CTTGAGCAAG	CGCAGGAACA	ACAGTACGTA	GAGGGCGGTG	GAGGCTCCCC	GGGTGAACCG	9240
TCTGGTCCAA	TCTCTACTAT	CAACCCGTCT	CCTCCGTCTA	AAGAATCTCA	TAAATCTCCA	9300
AACATGGCTG	AACTGGGAAT	GGCCCCTGCC	CTGCAGCCCA	CCCAGGGTGC	CATGCCGGCC	9360
TTGCCTCTG	CTTTCCAGCG	CCGGGCAGGA	GGGGTCCTGG	TTGCTAGCCA	TCTGCAGAGC	9420
TTCTTGAGG	TGTCGTACCG	CGTTCTACGC	CACCTTGCGC	AGCCCGACAT	GGCTACACCA	9480
TTAGGCCCTG	CCAGCTCCCT	GCCCCAGAGC	TTCTTGCTCA	AGTCTTTAGA	GCAAGTGAGG	9540
AAGATCCAGG	GCGATGGCGC	AGCGCTCCAG	GAGAAGCTGT	GTGCCACCTA	CAAGCTGTGC	9600
CACCCCGAGG	AGCTGGTGCT	GCTCGGACAC	TCTCTGGGCA	TCCCCTGGGC	TCCCCTGAGC	9660
TCCTGCCCCA	GCCAGGCCCT	GCAGCTGGCA	GGCTGCTTGA	GCCAACTCCA	TAGCGGCCTT	9720
TTCTCTTACC	AGGGGCTCCT	GCAGGCCCTG	GAAGGGATAT	CCCCCGAGTT	GGGTCCCACC	9780

TTGGACACAC	TGCAGCTGGA	CGTCGCCGAC	TTTGCCACCA	CCATCTGGCA	GCAGATGGAA	9840
ACGTACTCCA	TGGCTAACTG	CTCTATAATG	ATCGATGAAA	TTATACATCA	CTTAAAGAGA	9900
CCACCTGCAC	CTTTGCTGGA	CCCGAACAAC	CTCAATGACG	AAGACGTCTC	TATCCTGATG	9960
GATCGAAACC	TTCGACTTCC	AAACCTGGAG	AGCTTCGTAA	GGGCTGTCAA	GAACCTAGAA	10020
AATGCATCAG	GTATTGAGGC	AATTCTTCGT	AATCTCCAAC	CATGTCTGCC	CTCTGCCACG	10080
GCCGCACCCT	CTCGACATCC	AATCATCATC	AAGGCAGGTG	ACTGGCAAGA	ATTCCGGGAA	10140
AAACTGACGT	TCTATCTGGT	TACCCTTGAG	CAAGCGCAGG	AACAACAGTA	CGTAGAGGGC	10200
GGTGGAGGCT	CCCCGGGTGA	ACCGTCTGGT	CCAATCTCTA	CTATCAACCC	GTCTCCTCCG	10260
TCTAAAGAAT	CTCATAAATC	TCCAAACATG	GCTGGAATGG	CCCCTGCCCT	GCAGCCCACC	10320
CAGGGTGCCA	TGCCGGCCTT	CGCCTCTGCT	TTCCAGCGCC	GGGCAGGAGG	GGTCCTGGTT	10380
GCTAGCCATC	TGCAGAGCTT	CCTGGAGGTG	TCGTACCGCG	TTCTACGCCA	CCTTGCGCAG	10440
CCCGACATGG	CTACACCATT	AGGCCCTGCC	AGCTCCCTGC	CCCAGAGCTT	CCTGCTCAAG	10500
TCTTTAGAGC	AAGTGAGGAA	GATCCAGGGC	GATGGCGCAG	CGCTCCAGGA	GAAGCTGTGT	10560
GCCACCTACA	AGCTGTGCCA	CCCCGAGGAG	CTGGTGCTGC	TCGGACACTC	TCTGGGCATC	10620
CCCTGGGCTC	CCCTGAGCTC	CTGCCCCAGC	CAGGCCCTGC	AGCTGGCAGG	CTGCTTGAGC	10680
CAACTCCATA	GCGGCCTTTT	CCTCTACCAG	GGGCTCCTGC	AGGCCCTGGA	AGGGATATCC	10740
CCCGAGTTGG	GTCCCACCTT	GGACACACTG	CAGCTGGACG	TCGCCGACTT	TGCCACCACC	10800
ATCTGGCAGC	AGATGGAAGA	ACTGACGTAC	TCCATGGCTA	ACTGCTCTAT	AATGATCGAT	10860
GAAATTATAC	ATCACTTAAA	GAGACCACCT	GCACCTTTGC	TGGACCCGAA	CAACCTCAAT	10920
GACGAAGACG	TCTCTATCCT	GATGGATCGA	AACCTTCGAC	TTCCAAACCT	GGAGAGCTTC	10980
GTAAGGGCTG	TCAAGAACTT	AGAAAATGCA	TCAGGTATTG	AGGCAATTCT	TCGTAATCTC	11040
CAACCATGTC	TGCCCTCTGC	CACGGCCGCA	CCCTCTCGAC	ATCCAATCAT	CATCAAGGCA	11100
GGTGACTGGC	AAGAATTCCG	GGAAAACTG	ACGTTCTATC	TGGTTACCCT	TGAGCAAGCG	11160
CAGGAACAAC	AGTACGTAGA	GGGCGGTGGA	GGCTCCCCGG	GTGAACCGTC	TGGTCCAATC	11220
TCTACTATCA	ACCCGTCTCC	TCCGTCTAAA	GAATCTCATA	AATCTCCAAA	CATGGCTAGC	11280
TTCTGGAGG	TGTCGTACCG	CGTTCTACGC	CACCTTGCGC	AGCCCGACAT	GGCTACACCA	11340
TTAGGCCCTG	CCAGCTCCCT	GCCCCAGAGC	TTCTTGCTCA	AGTCTTTAGA	GCAAGTGAGG	11400
AAGATCCAGG	GCGATGGCGC	AGCGCTCCAG	GAGAAGCTGT	GTGCCACCTA	CAAGCTGTGC	11460
CACCCCGAGG	AGCTGGTGCT	GCTCGGACAC	TCTCTGGGCA	TCCCCTGGGC	TCCCCTGAGC	11520

TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT	11580
TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC	11640
TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA	11700
GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT	11760
GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAG	11808

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TTCATAAAT CTCCAAACAT GGCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG	480
AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC	540
CACCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC	600
TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT	660
TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC	720
TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA	780
GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT	840
GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG CTCCTGGAG	900



GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT	960
GCCAGCTCCC TGCCC	975

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 975 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG	480
AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC	540
CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC	600
TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT	660
TTCTCTTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC	720
TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA	780
GAACTGGGAA TGGCCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT	840
GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG	900
GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT	960
GCCAGCTCCC TGCCC	975

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 975 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG	480
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC	540
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG	600
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG	660
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	720
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG	780
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG	840
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC	900
CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC	960
CTGCTCAAGT CTTTA	975

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 975 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC	480
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC	540
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT	600
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG	660
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC	720
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC	780
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCGACATGGC TACACCATTA	840
GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG	900
ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC	960
CCCGAGGAGC TGGTG	975

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG	480
GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCTCT ACCAGGGGCT CCTGCAGGCC	540
CTGGAAGGGA TATCCCCCGA GTTEGGTCCC ACCTTGACA CACTGCAGCT GGACGTCGCC	600
GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG	660
CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC	720
CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCTG ACCGCGTTCT ACGCCACCTT	780
GCGCAGCCCG ACATGGCTAC ACCATTAGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG	840
CTCAAGTCTT TAGAGCAAGT GAGGAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG	900
CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG AACTCTCTG	960
GGCATCCCCCT GGGCT	975

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	480
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCGAG	540
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	600
CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	660
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	720
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGA CATGGCTACA	780
CCATTAGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG	840
AGGAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG	900
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG	960
AGCTCCTGCC CCAGC	975

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420

TCTCATAAAT CTCCAAACAT GGCTCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC	480
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT	540
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG	600
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC	660
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC	720
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCGACATGGC TACACCATTA	780
GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG	840
ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC	900
CCCAGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC	960
TGCCCCAGCC AGGCC	975

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT	480
TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC	540
TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA	600
GAAGTGGGAA TGGCCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT	660

GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG CTTCTGGAG	720
GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT	780
GCCAGCTCCC TGCCCCAGAG CTTCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG	840
GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG	900
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC	960
AGCCAGGCCC TGCA	975

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCAG	480
GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT	540
AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC TACGCCACCT TGCGCAGCCC	600
GACATGGCTA CACCATTAGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT	660
TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC	720
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC	780
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA	840

CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC	900
GAGTTGGGTC CCACCTTGA CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC	960
TGGCAGCAGA TGGAA	975

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTGGAATG GCCCCTGCCC TGCAGCCAC CCAGGGTGCC	480
ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT	540
CTGCAGAGCT TCCTGGAGGT GTCGTACCGC GTTCTACGCC ACCTTGCGCA GCCCGACATG	600
GCTACACCAT TAGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG	660
CAAGTGAGGA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC	720
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT	780
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT	840
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCAGATTG	900
GGTCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG	960
CAGATGGAAG AACTG	975

(2) INFORMATION FOR SEQ ID NO:270:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 975 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC	480
CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC	540
CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG	600
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT	660
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC	720
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA	780
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT	840
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCACC	900
CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTTGTT	960
GCTAGCCATC TGCAG	975

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 325 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	
1				5					10					15		
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	
			20					25					30			
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	
		35					40					45				
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	
	50					55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	
65					70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	
				85					90					95		
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	
			100					105					110			
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	
		115					120					125				
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	
	130					135					140					
Pro	Asn	Met	Ala	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	
145					150					155					160	
Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	
				165					170					175		
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	
			180					185					190			
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	
		195					200					205				
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	
	210					215					220					
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	
225					230					235					240	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	
				245					250					255		
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	
			260					265					270			

Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser
		275					280					285			
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln
	290					295					300				
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro
305					310					315					320
Asp	Met	Ala	Thr	Pro											
				325											

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75						80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro
		115					120					125			
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser
	130					135					140				
Pro	Asn	Met	Ala	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu
145					150					155					160

Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala  
 165 170 175  
 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu  
 180 185 190  
 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser  
 195 200 205  
 Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu  
 210 215 220  
 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly  
 225 230 235 240  
 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val  
 245 250 255  
 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met  
 260 265 270  
 Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser  
 275 280 285  
 Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln  
 290 295 300  
 Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
 305 310 315 320  
 Asp Met Ala Thr Pro  
 325

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45

Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	115	120	125
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140
Pro	Asn	Met	Ala	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	145	150	155
Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	165	170	175
Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	180	185	190
Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	195	200	205
Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	210	215	220
Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	225	230	235
Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	245	250	255
Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	260	265	270
Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	275	280	285
Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	290	295	300
Arg	His	Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	305	310	315
Ser	Leu	Pro	Gln	Ser												325		

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	115	120	125	
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140	
Pro	Asn	Met	Ala	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	145	150	155	160
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	165	170	175	
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	180	185	190	
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	195	200	205	
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	210	215	220	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	225	230	235	240

Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	245	250	255	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	260	265	270	
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	275	280	285	
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	290	295	300	
Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	305	310	315	320
Leu	Leu	Lys	Ser	Leu												325			

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro				

115		120		125
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser				
130		135		140
Pro Asn Met Ala Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro				
145		150		155
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser				
	165		170	175
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu				
	180		185	190
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu				
	195		200	205
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu				
	210		215	220
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe				
225		230		235
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His				
	245		250	255
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala				
	260		265	270
Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln				
	275		280	285
Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp				
	290		295	300
Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His				
305		310		315
Pro Glu Glu Leu Val				
	325			

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:



Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	115	120	125	
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140	
Pro	Asn	Met	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	145	150	155	160
Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	165	170	175	
Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	180	185	190	
Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	195	200	205	
Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	210	215	220	
Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	225	230	235	240
Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	245	250	255	
Leu	Arg	His	Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	260	265	270	
Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	275	280	285	
Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	290	295	300	

Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu  
 305 310 315 320

Gly Ile Pro Trp Ala  
 325

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
 130 135 140

Pro Asn Met Ala Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu  
 145 150 155 160

His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly  
 165 170 175

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val  
 180 185 190

Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	195	200	205	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	210	215	220	
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	225	230	235	240
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	245	250	255	
Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	260	265	270	
Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	275	280	285	
Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	290	295	300	
Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	305	310	315	320
Ser	Ser	Cys	Pro	Ser												325			

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80

Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg		
				85					90					95			
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln		
			100					105					110				
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro		
		115					120					125					
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser		
	130					135					140						
Pro	Asn	Met	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser		
145					150					155					160		
Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser		
			165						170					175			
Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp		
		180						185					190				
Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro		
		195					200					205					
Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe		
	210					215					220						
Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe		
225					230					235					240		
Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Asp	Met		
			245						250					255			
Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu		
		260						265					270				
Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu		
	275						280					285					
Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu		
	290					295					300						
Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser		
305					310					315					320		
Cys	Pro	Ser	Gln	Ala													
				325													

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	
1				5					10					15		
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	
			20					25					30			
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	
		35					40					45				
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	
	50					55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	
65					70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	
				85					90					95		
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	
			100					105					110			
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	
		115					120					125				
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	
		130				135					140					
Pro	Asn	Met	Ala	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	
145					150					155					160	
Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	
				165					170					175		
Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	
			180					185					190			
Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	
		195				200						205				
Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	
		210				215					220					
Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	
225					230					235					240	
Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	
				245					250					255		
Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	
			260					265					270			

Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu  
 275 280 285  
 Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu  
 290 295 300  
 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro  
 305 310 315 320  
 Ser Gln Ala Leu Gln  
 325

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125  
 Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
 130 135 140  
 Pro Asn Met Ala Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln  
 145 150 155 160



Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	
50						55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	
65					70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	
				85					90					95		
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	
			100					105					110			
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	
		115					120					125				
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	
130						135					140					
Pro	Asn	Met	Ala	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	
145					150					155					160	
Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	
				165					170					175		
Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	
			180					185					190			
Arg	His	Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	
		195					200					205				
Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	
210						215					220					
Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	
225					230					235					240	
Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	
				245					250					255		
Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	
			260					265						270		
Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	
		275					280					285				
Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	
	290					295					300					
Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	
305					310					315					320	
Gln	Met	Glu	Glu	Leu												
				325												

(2) INFORMATION FOR SEQ ID NO:282:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	115	120	125	
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140	
Pro	Asn	Met	Ala	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	145	150	155	160
Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	165	170	175	
Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	180	185	190	
Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	195	200	205	
Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	210	215	220	
Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly				

225		230		235		240									
Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu
				245					250					255	
Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr
			260					265						270	
Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met
		275					280					285			
Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met
	290					295					300				
Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val
305					310					315					320
Ala	Ser	His	Leu	Gln											
				325											

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "Xaa at position 7 is Ser or Ala;"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 112
- (D) OTHER INFORMATION: /note= "Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro, Phe, Trp, or Met;"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 113
- (D) OTHER INFORMATION: /note= "Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 114
- (D) OTHER INFORMATION: /note= "Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 115  
(D) OTHER INFORMATION: /note= "Xaa at position 115 is  
deleted or Gln, Gly, Ser, Thr, Tyr, or Asn;"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 151  
(D) OTHER INFORMATION: /note= "Xaa at position 151 is Ser  
or Ala;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Ser	Pro	Ala	Pro	Pro	Ala	Xaa	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	
1				5					10					15		
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	
			20					25					30			
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	
		35					40					45				
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	
	50					55					60					
Gly	Ala	Val	Thr	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln		
65				70				75						80		
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	
				85				90						95		
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Xaa	
		100					105					110				
Xaa	Xaa	Xaa	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	
		115					120					125				
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	
	130						135				140					
Val	Gly	Gly	Ser	Thr	Leu	Xaa	Val	Arg								
145					150											

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met	Ala	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	1	5	10	15
Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	20	25	30	
Gly	Gly	Ser	Thr	Leu	Ala	Val	Arg	Glu	Phe	Gly	Gly	Asn	Met	Ala	Ser	35	40	45	
Pro	Ala	Pro	Pro	Ala	Ala	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	50	55	60	
Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	65	70	75	80
Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	85	90	95	
Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	100	105	110	
Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	115	120	125	
Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	130	135	140	
Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	145	150	155	160
Pro Gln																			

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met	Ala	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	1	5	10	15
Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	20	25	30	
Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	35	40	45	

Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met
50						55					60				
Leu	Val	Gly	Gly	Ser	Thr	Leu	Ala	Val	Arg	Glu	Phe	Gly	Gly	Asn	Met
65					70					75				80	
Ala	Ser	Pro	Ala	Pro	Pro	Ala	Ala	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu
				85					90					95	
Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu
			100					105					110		
Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser
		115					120					125			
Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile
130						135					140				
Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly
145					150					155					160
Gln	Leu														

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Ala	Thr	Gly	Gly	Cys	Thr	Gly	Gly	Ala	Cys	Cys	Cys	Ala	Cys	Thr	Thr
1				5				10						15	
Gly	Cys	Cys	Thr	Cys	Thr	Cys	Ala	Thr	Cys	Cys	Cys	Thr	Cys	Cys	Thr
			20				25					30			
Gly	Gly	Gly	Gly	Cys	Ala	Gly	Cys	Thr	Thr	Thr	Cys	Thr	Gly	Gly	Ala
		35				40					45				
Cys	Ala	Gly	Gly	Thr	Cys	Cys	Gly	Thr	Cys	Thr	Cys	Cys	Thr	Cys	Cys
	50					55				60					
Thr	Thr	Gly	Gly	Gly	Gly	Cys	Cys	Cys	Thr	Gly	Cys	Ala	Gly	Ala	Gly
65					70					75					80

Cys	Cys	Thr	Cys	Cys	Thr	Thr	Gly	Gly	Ala	Ala	Cys	Cys	Cys	Ala	Gly	
				85					90					95		
Cys	Thr	Thr	Cys	Cys	Thr	Cys	Cys	Ala	Cys	Ala	Gly	Gly	Gly	Cys	Ala	
			100					105					110			
Gly	Gly	Ala	Cys	Cys	Ala	Cys	Ala	Gly	Cys	Thr	Cys	Ala	Cys	Ala	Ala	
		115					120					125				
Gly	Gly	Ala	Thr	Cys	Cys	Cys	Ala	Ala	Thr	Gly	Cys	Cys	Ala	Thr	Cys	
		130				135					140					
Thr	Thr	Cys	Cys	Thr	Gly	Ala	Gly	Cys	Thr	Thr	Cys	Cys	Ala	Ala	Cys	
		145			150				155						160	
Ala	Cys	Cys	Thr	Gly	Cys	Thr	Cys	Cys	Gly	Ala	Gly	Gly	Ala	Ala	Ala	
				165					170					175		
Gly	Gly	Thr	Gly													
			180													

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATGGCTGGCA GGACCACAGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC	60
CTGCTCCGAG GAAAGGTGCG TTTCCTGATG CTTGTAGGAG GGTCCACCCT CGCCGTCAGG	120
GAATTCGGCG GCAACATGGC GTCTCCGGCG CCGCCTGCTG CTGACCTCCG AGTCCTCAGT	180
AAACTGCTTC GTGACTCCCA TGTCTTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC	240
CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC	300
CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA	360
GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT	420
TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT	480
CCACAG	486

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 531 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG      60
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC      120
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG      180
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG      240
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC      300
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG      360
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG      420
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC      480
CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC C              531
```

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 531 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```
GAAGTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT      60
GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG CTTCTGAG      120
GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT      180
GCCAGCTCCC TGCCCCAGAG CTTCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG      240
GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG      300
```

GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC	360
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC	420
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA	480
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA A	531

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC	60
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG	120
TACCGCGTTC TACGCCACCT TGCGCAGCCC GACATGGCTA CACCATTAGG CCCTGCCAGC	180
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	240
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	300
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	360
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG	420
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG	480
CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT G	531

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```
TTCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG      60
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC      120
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA      180
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG      240
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC      300
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCCTGC CCTGCAGCCC      360
ACCCAGGGTG CCATGCCGGC CTTGCGCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG      420
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG      480
CAGCCCGACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG C              531
```

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGA CATGGCTACA      60
CCATTAGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG      120
AGGAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG      180
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG      240
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC      300
CTTTTCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC      360
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG      420
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCACCCAGG GTGCCATGCC GGCCTTCGCC      480
TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC CTGGTTGCTA GCCATCTGCA G              531
```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGA CATGGCTACA	60
CCATTAGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG	120
AGGAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG	180
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG	240
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC	300
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC	360
ACCTTGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG	420
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCACCCAGG GTGCCATGCC GGCCTTCGCC	480
TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC CTGGTTGCTA GCCATCTGCA G	531

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 531 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG	60
AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC	120
CACCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC	180
TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT	240
TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC	300

TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA	360
GAAGTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTGCCTCT	420
GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG CTTCTGGAG	480
GTGTCGTACC GCGTTCCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC A	531

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCTGA GTCCTGCCC CAGCCAGGCC	60
CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC	120
CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA CCTTGACAC ACTGCAGCTG	180
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT	240
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA	300
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA	360
CGCCACCTTG CGCAGCCCGA CATGGCTACA CCATTAGGCC CTGCCAGCTC CCTGCCCCAG	420
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC	480
CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT G	531

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT	60
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCAGATTG	120
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG	180
CAGATGGAAG AACTGGGAAT GGCCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC	240
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC	300
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCGACAT GGCTACACCA	360
TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG	420
AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC	480
CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC T	531

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG	60
GGGCTCCTGC AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCCACCTT GGACACACTG	120
CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGAATG	180
GGCCCTGCCC TGACGCCAC CCAGGGTGCC ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC	240
CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT CTGCAGAGCT TCCTGGAGGT GTCGTACCGC	300
GTTCTACGCC ACCTTGCGCA GCCCGACATG GCTACACCAT TAGGCCCTGC CAGCTCCCTG	360
CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGGA AGATCCAGGG CGATGGCGCA	420
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG	480
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG C	531

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC	60
CTGCAGGCCC TGAAGGGAT ATCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG	120
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT	180
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA	240
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA	300
CGCCACCTTG CGCAGCCCGA CATGGCTACA CCATTAGGCC CTGCCAGCTC CCTGCCCCAG	360
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC	420
CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA	480
CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC C	531

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 531 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCTTTTTC TCTACCAGGG GCTCCTGCAG	60
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC	120
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGAATGGC CCCTGCCCTG	180
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG	240
GTCTTGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC	300

CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC	360
CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG	420
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT	480
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA G	531

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	1	5	10	15
Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	20	25	30	
His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	35	40	45	
Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	50	55	60	
Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	65	70	75	80
Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	85	90	95	
Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	100	105	110	
Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	115	120	125	
Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	130	135	140	
Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	145	150	155	160
Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	165	170	175	
Pro																			

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 177 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	
1				5				10						15		
Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	
			20				25						30			
Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	
		35					40					45				
Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	
		50				55					60					
Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	
65					70					75					80	
Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	
				85					90					95		
Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	
			100					105						110		
Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	
			115				120						125			
Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	
			130			135					140					
Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	
145					150					155					160	
Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	
				165					170					175		
Glu																

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 177 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe
1				5					10					15	
Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His
			20					25					30		
Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala
		35					40					45			
Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln
	50						55				60				
Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp
65					70					75					80
Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His
			85						90					95	
Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala
			100					105					110		
Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu
		115					120						125		
Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala
	130					135					140				
Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln
145					150					155					160
Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu
			165						170					175	

Leu

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	
1				5					10					15		
Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	
			20					25					30			
Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	
		35					40					45				
Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	
	50					55					60					
Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	
65					70					75					80	
Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	
				85					90					95		
Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	
			100					105					110			
Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	
		115					120					125				
Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	
		130				135					140					
Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	
145					150					155					160	
Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	
				165					170					175		

Ser

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	1	5	10	15
Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	20	25	30	
Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	35	40	45	
Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	50	55	60	
Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	65	70	75	80
Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	85	90	95	
Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	100	105	110	
Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	115	120	125	
Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	130	135	140	
Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	145	150	155	160
Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	165	170	175	

Gln

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	1	5	10	15
Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	20	25	30	



Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu  
 65 70 75 80  
 Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu  
 85 90 95  
 Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala  
 100 105 110  
 Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu  
 115 120 125  
 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg  
 130 135 140  
 Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu  
 145 150 155 160  
 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr  
 165 170 175  
 Pro

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
 1 5 10 15  
 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
 20 25 30  
 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 35 40 45  
 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
 50 55 60  
 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
 65 70 75 80  
 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
 85 90 95

Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe
			100					105					110		
Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Asp	Met
		115					120					125			
Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu
	130					135					140				
Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu
145					150					155					160
Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu
			165						170					175	

Val

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu
1				5					10					15	
Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala
		20					25					30			
Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln
		35					40					45			
Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu
	50					55				60					
Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala
65					70					75				80	
Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser
			85						90					95	
His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu
		100						105					110		
Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro
		115						120				125			

Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly
130					135					140					
Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys
145				150					155						160
His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp
			165					170						175	

Ala

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu
1			5					10					15		
Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu
		20					25						30		
Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala
		35					40					45			
Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu
		50				55					60				
Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg
65					70					75					80
Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu
				85					90					95	
Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr
			100					105					110		
Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser
		115					120					125			
Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu
		130					135				140				
Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu
145						150				155					160

Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro  
165 170 175

Ser

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu  
1 5 10 15

Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly  
20 25 30

Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr  
35 40 45

Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro  
50 55 60

Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala  
65 70 75 80

Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser  
85 90 95

Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu  
100 105 110

Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu  
115 120 125

Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu  
130 135 140

Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly  
145 150 155 160

His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln  
165 170 175

Ala

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 177 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln
1				5					10					15	
Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr
			20					25					30		
Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp
		35					40					45			
Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln
		50				55					60				
Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly
65					70					75				80	
Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg
				85					90					95	
Val	Leu	Arg	His	Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro
			100					105					110		
Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val
			115				120					125			
Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala
	130					135					140				
Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser
145					150					155				160	
Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu
				165				170					175		
Gln															

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 177 amino acids  
    (B) TYPE: amino acid



(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

His	Leu	Ala	Gln	Pro	Asp	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser
1				5					10					15	
Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile
			20					25					30		
Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys
		35					40					45			
Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile
	50						55				60				
Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala
65					70					75					80
Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu
				85					90					95	
Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp
			100						105					110	
Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln
			115											125	
Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala
	130					135						140			
Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu
145					150					155					160
Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu
					165					170					175

Arg

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

CACCTTGCGC AGCCCGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC	60
TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	120
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	180
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA	240
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	300
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	360
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC	420
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG	480
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG C	531